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<110> Garman, Peter  
Garman, Jonathan David  
Candia III, Albert Frederick  
Arbor Vita Corporation

<120> CLASP-5 Transmembrane Protein

<130> 020054-000511US

<140> US 09/736,960

<141> 2000-12-13

<150> US 60/160,860

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<150> US 60/162,498

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<150> US 60/240,539

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<170> PatentIn Ver. 2.1

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Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys	
1975 1980 1985	
cca ata ttc aga gtt gag agt caa aag agg gac tcc ttc cac aga tct	6117
Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser	
1990 1995 2000	
agt ttc agg aaa tgt gaa acc cag ttg tca cag ggc agc taa	6159
Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser	
2005 2010 2015	
gaaaagccat cttcattcgt ggagactgtg gccctgcaac cctggagaag gacttgctgg	6219
tacttaaaaa atgggacatt tgccaccag gactgactgt acactcctg atcagccagc	6279
actctggaag ctttgggatc ccaggaacca tggaattatt cccaaatgga ctctgaccag	6339
atTTTTGCCA tactgggggg tggcgggatg gaggatgggt actcaggaat gactgcgtat	6399
ttattaaagt gtgtttttcc acaatgtacc aaacaaggca taagcagctt ctctgctga	6459
ctacaaaggg aagccttact acaattccaa aaatcatcat ggttggaaat ttgggaggag	6699

attatttgtg aacttggttac ccttttggtg atggtggact aattgctgta tagttatttt 6759  
 tgttttatta ttactgttac attaatTTaa catgcattta tagaagaata cattcaaagc 6819  
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 <223> full length human CLASP-5

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 Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro  
 35 40 45  
 His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val  
 50 55 60  
 Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr  
 65 70 75 80  
 Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu  
 85 90 95  
 Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg  
 100 105 110  
 His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala  
 115 120 125  
 Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn  
 130 135 140  
 Leu Leu Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu

Val Asp Gln Gln Asp Ala Val Gln Ile Asn Trp Val Trp Glu Lys Trp  
 180 185 190

Lys	Glu	His	Leu	Gly	Asn	Arg	Ile	Leu	Val	Lys	Leu	Leu	Thr	Leu	Lys	195	200	205
Phe	Glu	Ile	Glu	Ile	Glu	Pro	Leu	Phe	Ala	Ser	Ile	Ala	Leu	Tyr	Asp	210	215	220
Val	Lys	Glu	Arg	Lys	Lys	Ile	Ser	Glu	Asn	Phe	His	Cys	Asp	Leu	Asn	225	230	235
Ser	Asp	Gln	Phe	Lys	Gly	Phe	Leu	Arg	Ala	His	Thr	Pro	Ser	Val	Ala	245	250	255
Ala	Ser	Ser	Gln	Ala	Arg	Ser	Ala	Val	Phe	Ser	Val	Thr	Tyr	Pro	Ser	260	265	270
Ser	Asp	Ile	Tyr	Leu	Val	Val	Lys	Ile	Glu	Lys	Val	Leu	Gln	Gln	Gly	275	280	285
Asp	Ile	Gly	Asp	Cys	Ala	Glu	Pro	Tyr	Thr	Val	Ile	Lys	Glu	Ser	Asp	290	295	300
Gly	Gly	Lys	Ser	Lys	Glu	Lys	Ile	Glu	Lys	Leu	Lys	Leu	Gln	Ala	Glu	305	310	315
Ser	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	325	330	335
Pro	Ile	Ser	Leu	Ser	Ser	Phe	Phe	Asn	Val	Ser	Thr	Leu	Glu	Arg	Glu	340	345	350
Val	Thr	Asp	Val	Asp	Ser	Val	Val	Gly	Arg	Ser	Pro	Val	Gly	Glu	Arg	355	360	365
Arg	Thr	Leu	Ala	Gln	Ser	Arg	Arg	Leu	Ser	Glu	Arg	Ala	Leu	Ser	Leu	370	375	380
Glu	Glu	Asn	Gly	Val	Gly	Ser	Asn	Phe	Lys	Thr	Ser	Thr	Leu	Ser	Val	385	390	395
Ser	Ser	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu	405	410	415
Phe	Lys	Phe	Leu	Ala	Asp	Tyr	Lys	Arg	Ser	Ser	Ser	Leu	Gln	Arg	Arg	420	425	430
Val	Lys	Ser	Ile	Pro	Gly	Leu	Leu	Arg	Leu	Glu	Ile	Ser	Thr	Ala	Pro	435	440	445
Glu	Ile	Ile	Asn	Cys	Cys	Leu	Thr	Pro	Glu	Met	Leu	Pro	Val	Lys	Pro	450	455	460
Phe	Pro	Glu	Asn	Arg	Thr	Arg	Pro	His	Lys	Glu	Ile	Leu	Glu	Phe	Pro	465	470	475

Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn	515	520	525
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln	530	535	540
Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr	545	550	555
Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His	565	570	575
Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala	580	585	590
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn	595	600	605
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys	610	615	620
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln	625	630	635
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile	645	650	655
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu	660	665	670
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro	675	680	685
Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu	690	695	700
Leu	Lys	Leu	Ser	Ile	Ile	Cys	Leu	Asn	Ser	Ser	Arg	Leu	Glu	Pro	Leu	705	710	715
Val	Leu	Phe	Leu	His	Leu	Val	Leu	Asp	Lys	Leu	Phe	Gln	Leu	Ser	Val	725	730	735
Gln	Pro	Met	Val	Ile	Ala	Gly	Gln	Thr	Ala	Asn	Phe	Ser	Gln	Phe	Ala	740	745	750
Phe	Glu	Ser	Val	Val	Ala	Ile	Ala	Asn	Ser	Leu	His	Asn	Ser	Lys	Asp	755	760	765
Leu	Ser	Lys	Asp	Gln	His	Gly	Arg	Asn	Cys	Leu	Leu	Ala	Ser	Tyr	Val	770	775	780
His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser	785	790	795

Met Ser Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp  
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Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys  
850 855 860

Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser  
865 870 875 880

Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu  
885 890 895

Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln  
900 905 910

His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe  
915 920 925

Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr  
930 935 940

Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln  
945 950 955 960

Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu  
965 970 975

Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys  
980 985 990

Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met  
995 1000 1005

Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn  
1010 1015 1020

Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys  
1025 1030 1035 1040

Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp  
1045 1050 1055

Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln  
1060 1065 1070

His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp  
1075 1080 1085

Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala  
1090 1095 1100

Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys  
1105 1110 1115 1120

Pro Glu Val Val Val Val Val Val Val Val Val Val Val Val Val Val Val

Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala  
1155 1160 1165

Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe  
1170 1175 1180

Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln  
1185 1190 1195 1200

Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe  
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Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile  
1220 1225 1230

Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe  
1235 1240 1245

Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys  
1250 1255 1260

Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu  
1265 1270 1275 1280

Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg  
1285 1290 1295

Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu  
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Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu  
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Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn  
1330 1335 1340

Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile  
1345 1350 1355 1360

Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly  
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Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr  
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Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe  
1395 1400 1405

Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys  
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His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser  
1425 1430 1435 1440

His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser

Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg  
1475 1480 1485

Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln  
1490 1495 1500

Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn  
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Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro  
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Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala  
1540 1545 1550

Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His  
1555 1560 1565

Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala  
1570 1575 1580

Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr  
1585 1590 1595 1600

Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu  
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Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly  
1620 1625 1630

Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu  
1635 1640 1645

Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val  
1650 1655 1660

Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu  
1665 1670 1675 1680

Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp  
1685 1690 1695

Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg  
1700 1705 1710

Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe  
1715 1720 1725

Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg  
1730 1735 1740

Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val  
1745 1750 1755 1760

Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg  
 1795 1800 1805  
 Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu  
 1810 1815 1820  
 Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala  
 1825 1830 1835 1840  
 Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe  
 1845 1850 1855  
 Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr  
 1860 1865 1870  
 Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met  
 1875 1880 1885  
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 1890 1895 1900  
 Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro  
 1905 1910 1915 1920  
 Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe  
 1925 1930 1935  
 Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr  
 1940 1945 1950  
 Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys  
 1955 1960 1965  
 Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu  
 1970 1975 1980  
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<223> preliminary human CLASP-5 cDNA sequence

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Ala Ser Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser	
35 40 45	
tca ccg ggg ctc ctc ttc aca gaa ctg gct gct gcc ctg gat gcc gaa	192
Ser Pro Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu	
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ggg gaa gga atc agc gaa gta caa agg aaa gct gtc agt gca att cac	240
Gly Glu Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His	
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Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu	
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Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile	
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Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg	
115 120 125	
aga tac cgc acc agt ggc tcg gat gaa gaa caa gaa gga gcc ggt gcc	432
Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala	
130 135 140	
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Ile Thr Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu	
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Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn	
165 170 175	
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Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp	
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atc atg aaa aat gct gat cag agc ctc att agg aag tgg att gct gac	624
Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp	
195 200 205	
ctg cca tca acg cag ctc aac agg att tta gat cta ctt ttc atc tgt	672
Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys	
210 215 220	
gtg tta tgt ttt gag tat aag gga aaa cag agt tct gac aaa gtc agt	720
Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser	

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gct Ala	cca Pro	ggg Gly 275	aac Asn	gac Asp	cga Arg	ttt Phe	cca Pro 280	ggc Gly	cta Leu	aat Asn	gaa Glu	aat Asn	ttg Leu	aga Arg	tgg Trp	864
aag Lys	aaa Lys 290	gag Glu	cag Gln	aca Thr	cat His	tgg Trp 295	cgg Arg	caa Gln	gct Ala	aat Asn	gag Glu	aag Lys	cta Leu	gat Asp	aaa Lys	912
aca Thr 305	aag Lys	gcc Ala	gag Glu	tta Leu	gat Asp 310	caa Gln	gaa Glu	gcc Ala	ttg Leu	atc Ile 315	agt Ser	ggc Gly	aat Asn	ctg Leu	gct Ala 320	960
aca Thr	gaa Glu	gca Ala	cat His 325	tta Leu	atc Ile	atc Ile	ctg Leu	gat Asp	atg Met 330	cag Gln	gaa Glu	aac Asn	att Ile	atc Ile 335	cag Gln	1008
gcg Ala	agc Ser	tcg Ser	gct Ala 340	ctg Leu	gac Asp	tgt Cys	aaa Lys 345	gac Asp	agc Ser	ctg Leu	ctg Leu	gga Gly	ggt Cly	gtt Val	ctg Leu	1056
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gtc Val	ctg Leu	cac His	cac His 405	tgc Cys	agc Ser	agc Ser	agc Ser	atg Met	gat Asp 410	gtc Val	acc Thr	cgg Arg	agc Ser	caa Gln 415	gcc Ala	1248
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aat Asn	ttt Phe 435	gca Ala	aga Arg	gta Val	aag Lys	atg Met	caa Gln 440	gta Val	acc Thr	atg Met	tcc Ser	ctg Leu	gca Ala	tct Ser	ttg Leu	1344
gtg Val	gga Gly 450	aga Arg	gca Ala	cca Pro	gac Asp	ttt Phe 455	aat Asn	gaa Glu	gag Glu	cac His	ctg Leu 460	aga Arg	aga Arg	tcc Ser	ttg Leu	1392
agg Arg 465	aca Thr	att Ile	ttg Leu	gcc Ala	tat Tyr 470	tca Ser	gaa Glu	gag Glu	gac Asp	aca Thr 475	gcc Ala	atg Met	cag Gln	atg Met	act Thr 480	1440

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Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met	
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Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro	
515 520 525	
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Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys	
530 535 540	
aag aag tgc tac acg gag gct gcc atg tgc ctg gtg cac gcc gct gcg	1680
Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala	
545 550 555 560	
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Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro	
565 570 575	
gtg ggc agt gtc agc ttc cag aat att tct tcc aat gtg ctg gag gag	1776
Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu	
580 585 590	
tct gtg gtc tct gag gac acc ctg tca cct gac gag gat ggg gtg tgc	1824
Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys	
595 600 605	
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Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln	
610 615 620	
gcc gcg gag ctc ttc agc acg gga ggc tta tat gag aca gtt aat gag	1920
Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu	
625 630 635 640	
gtc tac aag ctg gtc atc ccc atc cta gaa gcg cat cga gaa ttc cgg	1968
Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg	
645 650 655	
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Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile	
660 665 670	
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Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly	
675 680 685	
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Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr	
690 695 700	
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Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu	
705 710 715	

gac tcc act cct gtg gac aaa acc aag ttg gat cct aac aag gcc tac	2256
Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr	
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Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys	
755 760 765	
gac agg gtc aca tac ttt gag aag aat ttc aac ctc cgg agg ttc atg	2352
Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met	
770 775 780	
tac acc acc ccg ttc acc ctg gag ggg cgg cct cgg gga gag ctg cat	2400
Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His	
785 790 795 800	
gag cag tac aga agg aac aca gtc ctg acc act atg cac gcc ttc ccc	2448
Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro	
805 810 815	
tac atc aag acc agg atc agc gtc atc cag aag gag gag ttt gtt ttg	2496
Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu	
820 825 830	
aca ccg att gaa gtt gcc att gaa gac atg aag aag aag acc ctg cag	2544
Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln	
835 840 845	
tta gca gtt gcc att aac cag gag ccg cct gat gca aag atg ctt cag	2592
Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln	
850 855 860	
atg gtg ctg caa ggc tct gtg gga gct act gta aat cag gga cca ctg	2640
Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu	
865 870 875 880	
gaa gta gcc caa gtg ttt ttg gct gaa att cct gct gat cca aaa ctc	2688
Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu	
885 890 895	
tat cga cat cac aac aag ttg agg tta tgc ttt aag gaa ttc atc atg	2736
Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met	
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aga tgt ggt gaa gct gta gag aaa aac aag cgt ctc atc acg gca gac	2784
Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp	
915 920 925	
cag agg gaa tat cag cag gaa ctc aaa aag aac tat aac aag cta aaa	2832
Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys	
930 935 940	
gag aac ctc agg cca atg atc gag cgg aaa att cca gaa ctg tac aag	2880
Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys	
945 950 955	



Ser	Pro	Gly	Leu	Leu	Phe	Thr	Glu	Leu	Ala	Ala	Ala	Leu	Asp	Ala	Glu	50	55	60
Gly	Glu	Gly	Ile	Ser	Glu	Val	Gln	Arg	Lys	Ala	Val	Ser	Ala	Ile	His	65	70	75
Ser	Leu	Leu	Ser	Ser	His	Asp	Leu	Asp	Pro	Arg	Cys	Val	Lys	Pro	Glu	85	90	95
Val	Lys	Val	Lys	Ile	Ala	Ala	Leu	Tyr	Leu	Pro	Leu	Val	Gly	Ile	Ile	100	105	110
Leu	Asp	Ala	Leu	Pro	Gln	Leu	Cys	Asp	Phe	Thr	Val	Ala	Asp	Thr	Arg	115	120	125
Arg	Tyr	Arg	Thr	Ser	Gly	Ser	Asp	Glu	Glu	Gln	Glu	Gly	Ala	Gly	Ala	130	135	140
Ile	Thr	Gln	Asn	Val	Ala	Leu	Ala	Ile	Ala	Gly	Asn	Asn	Phe	Asn	Leu	145	150	155
Lys	Thr	Ser	Gly	Ile	Val	Leu	Ser	Ser	Leu	Pro	Tyr	Lys	Gln	Tyr	Asn	165	170	175
Met	Leu	Asn	Ala	Asp	Thr	Thr	Arg	Asn	Leu	Met	Ile	Cys	Phe	Leu	Trp	180	185	190
Ile	Met	Lys	Asn	Ala	Asp	Gln	Ser	Leu	Ile	Arg	Lys	Trp	Ile	Ala	Asp	195	200	205
Leu	Pro	Ser	Thr	Gln	Leu	Asn	Arg	Ile	Leu	Asp	Leu	Leu	Phe	Ile	Cys	210	215	220
Val	Leu	Cys	Phe	Glu	Tyr	Lys	Gly	Lys	Gln	Ser	Ser	Asp	Lys	Val	Ser	225	230	235
Thr	Gln	Val	Leu	Gln	Lys	Ser	Arg	Asp	Val	Lys	Ala	Arg	Leu	Glu	Glu	245	250	255
Ala	Leu	Leu	Arg	Gly	Glu	Gly	Ala	Arg	Gly	Glu	Met	Met	Arg	Arg	Arg	260	265	270
Ala	Pro	Gly	Asn	Asp	Arg	Phe	Pro	Gly	Leu	Asn	Glu	Asn	Leu	Arg	Trp	275	280	285
Lys	Lys	Glu	Gln	Thr	His	Trp	Arg	Gln	Ala	Asn	Glu	Lys	Leu	Asp	Lys	290	295	300
Thr	Lys	Ala	Glu	Leu	Asp	Gln	Glu	Ala	Leu	Ile	Ser	Gly	Asn	Leu	Ala	305	310	315
Thr	Glu	Ala	His	Leu	Ile	Ile	Leu	Asp	Met	Gln	Glu	Asn	Ile	Ile	Gln	325	330	335

Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp  
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Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln  
385 390 395 400

Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala  
405 410 415

Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser  
420 425 430

Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu  
435 440 445

Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu  
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Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr  
465 470 475 480

Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile  
485 490 495

Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met  
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Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro  
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Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys  
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Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala  
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Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro  
565 570 575

Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu  
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Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys  
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Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln  
610 615 620

Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu  
625 630 635 640

Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg  
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Phe	Phe	Gly	Ser	Lys	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	690	695	700
Lys	Glu	Pro	Ala	Ile	Thr	Lys	Leu	Pro	Glu	Ile	Ser	His	Arg	Leu	Glu	705	710	715
Ala	Phe	Tyr	Gly	Gln	Cys	Phe	Gly	Ala	Glu	Phe	Val	Glu	Val	Ile	Lys	725	730	735
Asp	Ser	Thr	Pro	Val	Asp	Lys	Thr	Lys	Leu	Asp	Pro	Asn	Lys	Ala	Tyr	740	745	750
Ile	Gln	Ile	Thr	Phe	Val	Glu	Pro	Tyr	Phe	Asp	Glu	Tyr	Glu	Met	Lys	755	760	765
Asp	Arg	Val	Thr	Tyr	Phe	Glu	Lys	Asn	Phe	Asn	Leu	Arg	Arg	Phe	Met	770	775	780
Tyr	Thr	Thr	Pro	Phe	Thr	Leu	Glu	Gly	Arg	Pro	Arg	Gly	Glu	Leu	His	785	790	795
Glu	Gln	Tyr	Arg	Arg	Asn	Thr	Val	Leu	Thr	Thr	Met	His	Ala	Phe	Pro	805	810	815
Tyr	Ile	Lys	Thr	Arg	Ile	Ser	Val	Ile	Gln	Lys	Glu	Glu	Phe	Val	Leu	820	825	830
Thr	Pro	Ile	Glu	Val	Ala	Ile	Glu	Asp	Met	Lys	Lys	Lys	Thr	Leu	Gln	835	840	845
Leu	Ala	Val	Ala	Ile	Asn	Gln	Glu	Pro	Pro	Asp	Ala	Lys	Met	Leu	Gln	850	855	860
Met	Val	Leu	Gln	Gly	Ser	Val	Gly	Ala	Thr	Val	Asn	Gln	Gly	Pro	Leu	865	870	875
Glu	Val	Ala	Gln	Val	Phe	Leu	Ala	Glu	Ile	Pro	Ala	Asp	Pro	Lys	Leu	885	890	895
Tyr	Arg	His	His	Asn	Lys	Leu	Arg	Leu	Cys	Phe	Lys	Glu	Phe	Ile	Met	900	905	910
Arg	Cys	Gly	Glu	Ala	Val	Glu	Lys	Asn	Lys	Arg	Leu	Ile	Thr	Ala	Asp	915	920	925
Gln	Arg	Glu	Tyr	Gln	Gln	Glu	Leu	Lys	Lys	Asn	Tyr	Asn	Lys	Leu	Lys	930	935	940
Glu	Asn	Leu	Arg	Pro	Met	Ile	Glu	Arg	Lys	Ile	Pro	Glu	Leu	Tyr	Lys	945	950	955
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(ITAM) motif 1

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Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	Leu	Leu	Thr	Phe	
			20					25					30			
Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	
		35					40					45				
Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	
	50					55					60					
Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	Val	Ser	Ala	Asn	
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Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	Met	Gly	Arg	His	
			85					90						95		
Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	Pro	Leu	Leu	Lys	
			100					105					110			
Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	Asp	Gln	His	Leu	
		115					120					125				
His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	Gly	Ala	Gln	Ala	
	130					135					140					
Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	His	Ala	Met	Glu	
145					150					155					160	
Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	Asn	Gln	Leu	Phe	
			165						170					175		
Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Val	Ala	Val	Asn	Val	Thr		
			180					185					190			
Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	Glu	Gly	Leu	Glu	
		195					200					205				
Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	Ala	Glu	Pro	Tyr	
	210					215					220					
Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	Thr	Lys	Ser	Met	
225					230					235					240	

Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	275	280	285
Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	290	295	300
Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	305	310	315
Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	325	330	335
Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	340	345	350
Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	355	360	365
Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	370	375	380
Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	385	390	395
Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	405	410	415
Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	420	425	430
Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	435	440	445
Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	450	455	460
Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	465	470	475
Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	485	490	495
Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro	500	505	510
Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	515	520	525
Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile	530	535	540
Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	545	550	555
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Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu	595	600	605
Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn	610	615	620
Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val	625	630	635
Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	Arg	Asn	645	650	655
Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser	Gln	Thr	Leu	660	665	670
Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	675	680	685
Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	690	695	700
Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	705	710	715
Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	725	730	735
Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	740	745	750
Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	755	760	765
Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	770	775	780
Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	785	790	795
Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	805	810	815
Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	820	825	830
Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	835	840	845
Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu	Thr	850	855	860
Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp	865	870	875

Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	915	920	925
Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	930	935	940
Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	945	950	955
Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Gly	965	970	975
Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr	Pro	Asn	Ile	980	985	990
Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	Gln	Asp	Val	His	995	1000	1005
Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	Asp	Gly	1010	1015	1020
Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	Lys	Leu	1025	1030	1035
Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	Asp	Glu	Asp	1045	1050	1055
Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	1060	1065	1070
Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	1075	1080	1085
Asn	Val	Lys	Met	Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	1090	1095	1100
Asp	Ser	Lys	Tyr	Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro	Phe	Phe	1105	1110	1115
Asp	Glu	Lys	Glu	Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Ser	His	1125	1130	1135
Asn	Ile	Arg	Arg	Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	1140	1145	1150
Arg	Gln	Gly	Gly	Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	1155	1160	1165
Ala	Ile	His	Cys	Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	1170	1175	1180
Gln	His	His	Thr	Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	1185	1190	1195

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 Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val  
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 Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu  
 1265 1270 1275 1280  
 Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala  
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 Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln  
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 Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His  
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11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 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Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	145	150	155	160
Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	165	170	175	
Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	180	185	190	
Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	195	200	205	
Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	210	215	220	
Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	225	230	235	240
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	245	250	255	
Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	260	265	270	
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	275	280	285	
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	290	295	300	
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	305	310	315	320
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	325	330	335	
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	340	345	350	
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	355	360	365	
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	370	375	380	
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	385	390	395	400
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	405	410	415	
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	420	425	430	

Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn	
465					470					475					480	
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	
				485					490					495		
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	
			500					505					510			
Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	
		515					520					525				
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	
	530					535					540					
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	
545					550					555					560	
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	
				565					570					575		
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	
			580					585					590			
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	
		595					600					605				
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	
	610					615					620					
Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	
625					630					635					640	
Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	
				645					650					655		
Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	
			660					665					670			
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	
		675					680					685				
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	
	690					695					700					
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	
705					710					715					720	
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	
				725					730					735		
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	
			740					745					750			

Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe  
785 790 795 800

Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg  
805 810 815

Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly  
820 825 830

Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp  
835 840 845

Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu  
850 855 860

Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe  
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Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys  
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Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr  
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Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe  
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Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys  
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Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr  
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Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr  
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Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser  
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Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe  
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Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg  
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Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn  
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Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr  
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His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val  
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 1140 1145 1150  
 Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly  
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Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly  
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Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg  
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Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe  
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Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys  
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Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn  
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Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe  
35 40 45

Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu  
50 55 60

Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln  
65 70 75 80

Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys  
85 90 95

Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu  
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Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu  
115 120 125

145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200

Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Asn	Asp	Pro	Glu	Met	
				165					170					175		
Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	Ala	Ser	Thr	Pro	
			180					185					190			
Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Arg	Ile	His	Val	Lys	
		195					200					205				
Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	His	Val	Thr	Ala	
	210					215					220					
Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Glu	Ala	Asp	Leu	Ala	Leu	Gln	
225					230					235					240	
Arg	Glu	Pro	Pro	Val	Phe	Pro	Tyr	Ser	His	Thr	Ser	Cys	Gln	Arg	Lys	
				245					250					255		
Ser	Arg	Gly	Gly	Met	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	
			260					265					270			
Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	
		275					280					285				
Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	
	290					295					300					
Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Leu	Arg	Ala	Gly	Leu	Leu	
305					310					315					320	
Thr	Ser	Ile	Asn	Ser	Ser	Ser	Pro	Ser	Met	Lys	Ser	Gly	Gly	Thr	Leu	
			325						330					335		
Glu	Thr	Thr	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Pro	Tyr	Ser	Lys	Val	
			340					345					350			
Thr	Glu	Val	Ile	Thr	Arg	Ala	Ala	Gly	Ser	Trp	Asp	Leu	Leu	Pro	Gly	
		355					360					365				
Gly	Leu	Phe	Gly	Gln	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr	
	370					375					380					
Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg	
385					390					395					400	
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met	
				405					410					415		
Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Phe	
			420					425					430			
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Thr	Pro	Phe	Phe	Asp	Glu	Lys	Glu	
		435					440					445				

Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys	
				485					490					495		
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr	
			500					505					510			
Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val	
		515					520					525				
Ala	Glu	Leu	His	Gln	Leu	Cys	Ser	Ser	Ala	Glu	Val	Asp	Met	Ile	Lys	
	530					535					540					
Leu	Gln	Leu	Lys	Leu	Gln	Gly	Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly	
545					550					555					560	
Pro	Leu	Ala	Tyr	Ala	Arg	Ala	Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg	
				565					570					575		
Tyr	Pro	Asp	Asn	Lys	Val	Lys	Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe	
			580					585					590			
Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	Val	Asn	Glu	Arg	Leu	Ile	Lys	
		595					600					605				
Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	Met	Lys	Ala	Asn	Tyr	Arg	Glu	
	610					615					620					
Ile	Arg	Lys	Glu	Leu	Ser	Asp	Ile	Ile	Val	Pro	Arg	Ile	Cys	Pro	Gly	
625					630					635					640	
Glu	Asp	Lys	Arg	Ala	Thr	Lys	Phe	Pro	Ala	His	Leu	Gln	Arg	His	Gln	
				645					650					655		
Arg	Asp	Thr	Asn	Lys	His	Ser	Gly	Ser	Arg	Val	Asp	Gln	Phe	Ile	Leu	
			660					665					670			
Ser	Cys	Val	Thr	Leu	Pro	His	Glu	Pro	His	Val	Gly	Thr	Cys	Phe	Val	
		675					680					685				
Met	Cys	Lys	Leu	Arg	Thr	Thr	Phe	Arg	Ala	Asn	His	Trp	Phe	Cys	Gln	
	690					695					700					
Ala	Gln	Glu	Glu	Ala	Met	Gly	Asn	Gly	Arg	Glu	Lys	Glu	Pro	Trp	Thr	
705					710					715					720	
Val	Ile	Phe	Asn	Ser	Arg	Phe	Tyr	Arg	Ser	Trp	Gly	Lys	Val	His	Ile	
				725					730					735		

Phe Phe

<210> 12

<211> 1214

<212> PRT

<400> 12

Met	Glu	Ile	Gln	Val	Leu	Ile	Arg	Phe	Leu	Ser	Val	Ile	Leu	Met	Gln
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Leu	Phe	Trp	Val	Leu	Pro	Asn	Met	Ile	His	Glu	Asp	Asp	Val	Pro	Ile
			20					25					30		
Ser	Cys	Pro	Met	Val	Leu	Phe	His	Ile	Val	Ser	Lys	Cys	His	Glu	Glu
		35					40					45			
Gly	Leu	Asp	Ser	Tyr	Leu	Ser	Ser	Phe	Ile	Lys	Tyr	Ser	Phe	Arg	Pro
	50					55					60				
Gly	Lys	Pro	Ser	Ala	Pro	Gln	Ala	Pro	Leu	Ile	His	Glu	Thr	Leu	Ala
65					70					75					80
Thr	Met	Met	Ile	Ala	Leu	Leu	Lys	Gln	Ser	Ala	Asp	Phe	Leu	Ala	Ile
				85					90					95	
Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Glu	Ile	Ile	Ala	Lys
			100					105					110		
Ser	Met	Ala	Thr	Tyr	Leu	Leu	Glu	Glu	Asn	Lys	Ile	Lys	Leu	Thr	His
		115					120					125			
Gly	Gln	Arg	Phe	Pro	Lys	Ala	Tyr	His	His	Ala	Leu	His	Ser	Leu	Phe
	130					135					140				
Leu	Ala	Ile	Thr	Ile	Val	Glu	Ser	Gln	Tyr	Ala	Glu	Ile	Pro	Lys	Glu
145					150					155					160
Ser	Arg	Asn	Val	Asn	Tyr	Ser	Leu	Ala	Ser	Phe	Leu	Lys	Cys	Cys	Leu
			165						170					175	
Thr	Leu	Met	Asp	Arg	Gly	Phe	Val	Phe	Asn	Leu	Ile	Asn	Asp	Tyr	Ile
		180						185					190		
Ser	Gly	Phe	Ser	Pro	Lys	Asp	Pro	Lys	Val	Leu	Ala	Glu	Tyr	Lys	Phe
	195						200					205			
Glu	Phe	Leu	Gln	Thr	Ile	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn
	210					215					220				
Leu	Pro	Met	Ala	Phe	Ala	Lys	Pro	Lys	Leu	Gln	Arg	Val	Gln	Asp	Ser
225					230					235					240
Asn	Leu	Glu	Tyr	Ser	Leu	Ser	Asp	Glu	Tyr	Cys	Lys	His	His	Phe	Leu
				245					250					255	
Val	Gly	Leu	Leu	Leu	Arg	Glu	Thr	Ser	Ile	Ala	Leu	Gln	Asp	Asn	Tyr
		260						265					270		
Glu	Ile	Arg	Tyr	Thr	Ala	Ile	Ser	Val	Ile	Lys	Asn	Leu	Leu	Ile	Lys
		275					280					285			

Arg	Leu	Ala	Gly	Arg	Asp	Thr	Leu	Tyr	Ser	Cys	Ala	Ala	Met	Pro	Asn	325	330	335	
Ser	Ala	Ser	Arg	Asp	Glu	Phe	Pro	Cys	Gly	Phe	Thr	Ser	Pro	Ala	Asn	340	345	350	
Arg	Gly	Ser	Leu	Ser	Thr	Asp	Lys	Asp	Thr	Ala	Tyr	Gly	Ser	Phe	Gln	355	360	365	
Asn	Gly	His	Gly	Ile	Lys	Arg	Glu	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Pro	370	375	380	
Glu	Gly	Ala	Thr	Gly	Phe	Pro	Asp	Gln	Gly	Asn	Thr	Gly	Glu	Asn	Thr	385	390	395	400
Arg	Gln	Ser	Ser	Thr	Arg	Ser	Ser	Val	Ser	Gln	Tyr	Asn	Arg	Leu	Asp	405	410	415	
Gln	Tyr	Glu	Ile	Arg	Ser	Leu	Leu	Met	Cys	Tyr	Leu	Tyr	Ile	Val	Lys	420	425	430	
Met	Ile	Ser	Glu	Asp	Thr	Leu	Leu	Thr	Tyr	Trp	Asn	Lys	Val	Ser	Pro	435	440	445	
Gln	Glu	Leu	Ile	Asn	Ile	Leu	Ile	Leu	Leu	Glu	Val	Cys	Leu	Phe	His	450	455	460	
Phe	Arg	Tyr	Met	Gly	Lys	Arg	Asn	Ile	Ala	Arg	Val	His	Asp	Ala	Trp	465	470	475	480
Leu	Ser	Lys	His	Phe	Gly	Ile	Asp	Arg	Lys	Ser	Gln	Thr	Met	Pro	Ala	485	490	495	
Leu	Arg	Asn	Arg	Ser	Gly	Val	Met	Gln	Ala	Arg	Leu	Gln	His	Leu	Ser	500	505	510	
Ser	Leu	Glu	Ser	Ser	Phe	Thr	Leu	Asn	His	Ser	Ser	Thr	Thr	Thr	Glu	515	520	525	
Ala	Asp	Ile	Phe	His	Gln	Ala	Leu	Leu	Glu	Gly	Asn	Thr	Ala	Thr	Glu	530	535	540	
Val	Ser	Leu	Thr	Val	Leu	Asp	Thr	Ile	Ser	Phe	Phe	Thr	Gln	Cys	Phe	545	550	555	560
Lys	Thr	His	Phe	Leu	Asn	Asn	Asp	Gly	His	Asn	Pro	Leu	Met	Lys	Lys	565	570	575	
Val	Phe	Asp	Ile	His	Leu	Ala	Phe	Leu	Lys	Asn	Gly	Gln	Ser	Glu	Val	580	585	590	
Ser	Leu	Lys	His	Val	Phe	Ala	Ser	Leu	Arg	Ala	Phe	Ile	Ser	Lys	Phe	595	600	605	

Glu	Ala	Ser	Ala	Leu	Leu	Tyr	Leu	Leu	Met	Arg	Asn	Asn	Phe	Glu	Tyr	645	650	655
Thr	Lys	Arg	Lys	Thr	Phe	Leu	Arg	Thr	His	Leu	Gln	Ile	Ile	Ile	Ala	660	665	670
Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Ala	Leu	Ser	Gly	Gly	Ser	Arg	Phe	675	680	685
Gln	Glu	Ser	Leu	Phe	Ile	Ile	Asn	Asn	Phe	Ala	Asn	Ser	Asp	Arg	Pro	690	695	700
Met	Leu	Ala	Arg	Ala	Phe	Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	705	710	715
Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	725	730	735
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	740	745	750
Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Lys	755	760	765
Ile	His	Val	Lys	Asn	Gly	Asp	Phe	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	770	775	780
His	Val	Ala	Ala	Leu	Val	Ala	Glu	Phe	Leu	His	Arg	Lys	Lys	Leu	Phe	785	790	795
Pro	Asn	Gly	Cys	Ser	Ala	Phe	Lys	Lys	Ile	Thr	Pro	Asn	Ile	Asp	Glu	805	810	815
Glu	Gly	Ala	Met	Lys	Glu	Asp	Ala	Gly	Met	Met	Asp	Val	His	Tyr	Ser	820	825	830
Glu	Glu	Val	Leu	Leu	Glu	Leu	Leu	Glu	Gln	Cys	Val	Asn	Gly	Leu	Trp	835	840	845
Lys	Ala	Glu	Arg	Tyr	Glu	Ile	Ile	Ser	Glu	Ile	Ser	Lys	Leu	Ile	Gly	850	855	860
Pro	Ile	Tyr	Glu	Asn	Arg	Arg	Glu	Phe	Glu	Asn	Leu	Thr	Gln	Val	Tyr	865	870	875
Arg	Thr	Leu	His	Gly	Ala	Tyr	Thr	Lys	Ile	Leu	Glu	Val	Met	His	Thr	885	890	895
Lys	Lys	Arg	Leu	Leu	Gly	Thr	Phe	Phe	Arg	Val	Ala	Phe	Tyr	Gly	Gln	900	905	910
Ser	Phe	Phe	Glu	Glu	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	915	920	925

Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val  
 965 970 975  
 Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys  
 980 985 990  
 Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala  
 995 1000 1005  
 Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys  
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 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys  
 1025 1030 1035 1040  
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile  
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 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys  
 1060 1065 1070  
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu  
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 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala  
 1090 1095 1100  
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys  
 1105 1110 1115 1120  
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser  
 1125 1130 1135  
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu  
 1140 1145 1150  
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu  
 1155 1160 1165  
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser  
 1170 1175 1180  
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 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val  
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<210> 13  
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 <212> PRT  
 <213> Homo sapiens

Gln	Asn	Glu	Glu	Asp	Glu	Ile	Thr	Thr	Thr	Val	Thr	Arg	Val	Leu	Pro	20	25	30
Asp	Ile	Val	Ala	Lys	Cys	His	Glu	Glu	Gln	Leu	Asp	His	Ser	Val	Gln	35	40	45
Ser	Tyr	Ile	Lys	Phe	Val	Phe	Lys	Thr	Arg	Ala	Cys	Lys	Glu	Arg	Pro	50	55	60
Val	His	Glu	Asp	Leu	Ala	Lys	Asn	Val	Thr	Gly	Leu	Leu	Lys	Ser	Asn	65	70	75
Asp	Ser	Pro	Thr	Val	Lys	His	Val	Leu	Lys	His	Ser	Trp	Phe	Phe	Phe	85	90	95
Ala	Ile	Ile	Leu	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Asp	Thr	Asn	Lys	100	105	110
Ile	Gln	Leu	Pro	Arg	Pro	Gln	Arg	Phe	Pro	Glu	Ser	Tyr	Gln	Asn	Glu	115	120	125
Leu	Asp	Asn	Leu	Val	Met	Val	Leu	Ser	Asp	His	Val	Ile	Trp	Lys	Tyr	130	135	140
Lys	Asp	Ala	Leu	Glu	Glu	Thr	Arg	Arg	Ala	Thr	His	Ser	Val	Ala	Arg	145	150	155
Phe	Leu	Lys	Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Cys	Val	Phe	Lys	165	170	175
Met	Val	Asn	Asn	Tyr	Ile	Ser	Met	Phe	Ser	Ser	Gly	Asp	Leu	Lys	Thr	180	185	190
Leu	Cys	Gln	Tyr	Lys	Phe	Asp	Phe	Leu	Gln	Glu	Val	Cys	Gln	His	Glu	195	200	205
His	Phe	Ile	Pro	Leu	Cys	Leu	Pro	Ile	Arg	Ser	Ala	Asn	Ile	Pro	Asp	210	215	220
Pro	Leu	Thr	Pro	Ser	Glu	Ser	Thr	Gln	Glu	Leu	His	Ala	Ser	Asp	Met	225	230	235
Pro	Glu	Tyr	Ser	Val	Thr	Asn	Glu	Phe	Cys	Arg	Lys	His	Phe	Leu	Ile	245	250	255
Gly	Ile	Leu	Leu	Arg	Glu	Val	Gly	Phe	Ala	Leu	Gln	Glu	Asp	Gln	Asp	260	265	270
Val	Arg	His	Leu	Ala	Leu	Ala	Val	Leu	Lys	Asn	Leu	Met	Ala	Lys	His	275	280	285
Ser	Phe	Asp	Asp	Arg	Tyr	Arg	Glu	Pro	Arg	Lys	Gln	Ala	Gln	Ile	Ala	290	295	300
Ser	Leu	Thr	Met	Val	Leu	Thr	Thr	Met	Val	Lys	Leu	Met	Val	Pro	Leu	305	310	315

Gly	Ser	Arg	Asp	Asp	Leu	Ser	Thr	Asn	Gly	Gly	Phe	Gln	Ser	Gln	Thr	340	345	350
Ala	Ile	Lys	His	Ala	Asn	Ser	Val	Asp	Thr	Ser	Phe	Ser	Lys	Asp	Val	355	360	365
Leu	Asn	Ser	Ile	Ala	Ala	Phe	Ser	Ser	Ile	Ala	Ile	Ser	Thr	Val	Asn	370	375	380
His	Ala	Asp	Ser	Arg	Ala	Ser	Leu	Ala	Ser	Leu	Asp	Ser	Asn	Pro	Ser	385	390	395
Thr	Asn	Glu	Lys	Ser	Ser	Glu	Lys	Thr	Asp	Asn	Cys	Glu	Lys	Ile	Pro	405	410	415
Arg	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Leu	Arg	Phe	Asp	Arg	Leu	Asp	420	425	430
Gln	Ala	Glu	Thr	Arg	Ser	Leu	Leu	Met	Cys	Phe	Leu	His	Ile	Met	Lys	435	440	445
Thr	Ile	Ser	Tyr	Glu	Thr	Leu	Ile	Ala	Tyr	Trp	Gln	Arg	Ala	Pro	Ser	450	455	460
Pro	Glu	Val	Ser	Asp	Phe	Phe	Ser	Ile	Leu	Asp	Val	Cys	Leu	Gln	Asn	465	470	475
Phe	Arg	Tyr	Leu	Gly	Lys	Arg	Asn	Ile	Ile	Arg	Lys	Ile	Ala	Ala	Ala	485	490	495
Phe	Lys	Phe	Val	Gln	Ser	Thr	Gln	Asn	Asn	Gly	Thr	Leu	Lys	Gly	Ser	500	505	510
Asn	Pro	Ser	Cys	Gln	Thr	Ser	Gly	Leu	Leu	Ala	Gln	Trp	Met	His	Ser	515	520	525
Thr	Ser	Arg	His	Glu	Gly	His	Lys	Gln	His	Arg	Ser	Gln	Thr	Leu	Pro	530	535	540
Ile	Ile	Arg	Gly	Lys	Asn	Ala	Leu	Ser	Asn	Pro	Lys	Leu	Leu	Gln	Met	545	550	555
Leu	Asp	Asn	Thr	Met	Thr	Ser	Asn	Ser	Asn	Glu	Ile	Asp	Ile	Val	His	565	570	575
His	Val	Asp	Thr	Glu	Ala	Asn	Ile	Ala	Thr	Glu	Gly	Cys	Leu	Thr	Ile	580	585	590
Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln	595	600	605
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr	610	615	620

Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys	660	665	670	
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu	675	680	685	
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser	690	695	700	
Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile	705	710	715	720
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile	725	730	735	
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe	740	745	750	
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	755	760	765	
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val	770	775	780	
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	785	790	795	800
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly	805	810	815	
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile	820	825	830	
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys	835	840	845	
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser	850	855	860	
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro	865	870	875	880
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys	885	890	895	
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val	900	905	910	
Glu	Gln	Leu	Tyr	Met	Cys	Gly	Glu	Phe	Leu	Trp	Lys	Ser	Glu	Arg	Tyr	915	920	925	
Glu	Leu	Ile	Ala	Asp	Val	Asn	Lys	Pro	Ile	Ile	Ala	Val	Phe	Glu	Lys	930	935	940	

Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu  
 980 985 990  
 Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu  
 995 1000 1005  
 Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly  
 1010 1015 1020  
 Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys  
 1025 1030 1035 1040  
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro  
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 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met  
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 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser  
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 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile  
 1090 1095 1100  
 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val  
 1105 1110 1115 1120  
 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp  
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 1155 1160 1165  
 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu  
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<212> PRT  
<213> Homo sapiens

<220>  
<223> human CLASP-3

<400> 14

Gly	Pro	Gly	Pro	Ala	Arg	Ser	Thr	Val	Ser	Ile	Ser	Leu	Ile	Ser	Asn	
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Ser	Ala	Arg	Val	Asn	Arg	Ser	Arg	Ser	Leu	Ser	Asn	Ser	Asn	Pro	Asp	
			20					25					30			
Ile	Ser	Gly	Thr	Pro	Thr	Ser	Pro	Asp	Asp	Glu	Val	Arg	Ser	Ile	Ile	
		35					40					45				
Gly	Ser	Lys	Gly	Leu	Asp	Arg	Ser	Asn	Ser	Trp	Val	Asn	Thr	Gly	Gly	
	50					55					60					
Pro	Lys	Ala	Ala	Pro	Trp	Gly	Ser	Asn	Pro	Ser	Pro	Ser	Ala	Glu	Ser	
65					70					75					80	
Thr	Gln	Ala	Met	Asp	Arg	Ser	Cys	Asn	Arg	Met	Ser	Ser	His	Thr	Glu	
			85						90					95		
Thr	Ser	Ser	Phe	Leu	Gln	Thr	Leu	Thr	Gly	Arg	Leu	Pro	Thr	Lys	Lys	
			100					105					110			
Leu	Phe	His	Glu	Glu	Leu	Ala	Leu	Gln	Trp	Val	Val	Cys	Ser	Gly	Ser	
	115						120					125				
Val	Arg	Glu	Ser	Ala	Leu	Gln	Gln	Ala	Trp	Phe	Phe	Phe	Glu	Leu	Met	
	130					135						140				
Val	Lys	Ser	Met	Val	His	His	Leu	Tyr	Phe	Asn	Asp	Lys	Leu	Glu	Ala	
145					150					155					160	
Pro	Arg	Lys	Ser	Arg	Phe	Pro	Glu	Arg	Phe	Met	Asp	Asp	Ile	Ala	Ala	
				165					170					175		
Leu	Val	Ser	Thr	Ile	Ala	Ser	Asp	Ile	Val	Ser	Arg	Phe	Gln	Lys	Asp	
			180					185					190			
Thr	Glu	Met	Val	Glu	Arg	Leu	Asn	Thr	Ser	Leu	Ala	Phe	Phe	Leu	Asn	
	195						200					205				
Asp	Leu	Leu	Ser	Val	Met	Asp	Arg	Gly	Phe	Val	Phe	Ser	Leu	Ile	Lys	
	210					215					220					
Ser	Cys	Tyr	Lys	Gln	Val	Ser	Ser	Lys	Leu	Tyr	Ser	Leu	Pro	Asn	Pro	
225					230					235					240	

Pro	Ala	Ser	Pro	Ser	Pro	Ser	Val	Ser	Ser	Ala	Thr	Ser	Gln	Ser	Ser	275	280	285
Gly	Phe	Ser	Thr	Asn	Val	Gln	Asp	Gln	Lys	Ile	Ala	Asn	Met	Phe	Glu	290	295	300
Leu	Ser	Val	Pro	Phe	Arg	Gln	Gln	His	Tyr	Leu	Ala	Gly	Leu	Val	Leu	305	310	315
Thr	Glu	Leu	Ala	Val	Ile	Leu	Asp	Pro	Asp	Ala	Glu	Gly	Leu	Phe	Gly	325	330	335
Leu	His	Lys	Lys	Val	Ile	Asn	Met	Val	His	Asn	Leu	Leu	Ser	Ser	His	340	345	350
Asp	Ser	Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala	355	360	365
Met	Leu	Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln	370	375	380
Leu	Tyr	Asp	Phe	Thr	Glu	Thr	His	Asn	Gln	Arg	Gly	Arg	Pro	Ile	Cys	385	390	395
Ile	Ala	Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln	405	410	415
Thr	Val	Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg	420	425	430
Pro	Gly	Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr	435	440	445
Phe	Ser	Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val	450	455	460
Leu	Lys	Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu	465	470	475
Ser	Val	Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val	485	490	495
Ser	Cys	Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser	500	505	510
Leu	Thr	Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala	515	520	525
Ile	Leu	Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg	530	535	540
Gly	Gln	Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu	545	550	555
																560		

Gly	Asn	Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu	595	600	605	
Ile	Val	Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu	610	615	620	
Gly	Gly	Val	Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser	625	630	635	640
Ala	Val	Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	645	650	655	
Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp	660	665	670	
Leu	Cys	Leu	Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile	675	680	685	
Arg	Ser	His	Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	690	695	700	
Glu	Ile	Gly	Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser	705	710	715	720
Leu	Ser	Ser	Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu	725	730	735	
Arg	Arg	Ser	Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu	740	745	750	
Leu	Arg	Glu	Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn	755	760	765	
Leu	His	Met	Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	770	775	780	
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr	785	790	795	800
Gln	Thr	Ser	Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	805	810	815	
Lys	His	Ser	Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val	820	825	830	
His	Ser	Ala	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg	835	840	845	
Lys	Tyr	Leu	Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn	850	855	860	
Val	Leu	Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	865	870	875	880

Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn	915	920	925
Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala	930	935	940
Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly	945	950	955
Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp	965	970	975
Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu	980	985	990
Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp	995	1000	1005
Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu	1010	1015	1020
Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe	1025	1030	1035
Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr	1045	1050	1055
Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg	1060	1065	1070
Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr	1075	1080	1085
Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His	1090	1095	1100
Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met	1105	1110	1115
Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala	1125	1130	1135
Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr	1140	1145	1150
Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile	1155	1160	1165
Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys	1170	1175	1180
Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys	1185	1190	1195
			1200

<210> 15

<211> 987

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-5

<400> 15

Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser  
1 5 10 15

Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser  
20 25 30

Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro  
35 40 45

Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu  
50 55 60

Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu  
65 70 75 80

Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys  
85 90 95

Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp  
100 105 110

Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr  
115 120 125

Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr  
130 135 140

Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr  
145 150 155 160

Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu  
165 170 175

Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met  
180 185 190

Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro  
195 200 205

Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu  
210 215 220

Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln  
225 230 235 240

Gly	Asn	Asp	Arg	Phe	Pro	Gly	Leu	Asn	Glu	Asn	Leu	Arg	Trp	Lys	Lys	275	280	285	
Glu	Gln	Thr	His	Trp	Arg	Gln	Ala	Asn	Glu	Lys	Leu	Asp	Lys	Thr	Lys	290	295	300	
Ala	Glu	Leu	Asp	Gln	Glu	Ala	Leu	Ile	Ser	Gly	Asn	Leu	Ala	Thr	Glu	305	310	315	320
Ala	His	Leu	Ile	Ile	Leu	Asp	Met	Gln	Glu	Asn	Ile	Ile	Gln	Ala	Ser	325	330	335	
Ser	Ala	Leu	Asp	Cys	Lys	Asp	Ser	Leu	Leu	Gly	Gly	Val	Leu	Arg	Val	340	345	350	
Leu	Val	Asn	Ser	Leu	Asn	Cys	Asp	Gln	Ser	Thr	Thr	Tyr	Leu	Thr	His	355	360	365	
Cys	Phe	Ala	Thr	Leu	Arg	Ala	Leu	Ile	Ala	Lys	Phe	Gly	Asp	Leu	Leu	370	375	380	
Phe	Glu	Glu	Glu	Val	Glu	Gln	Cys	Phe	Asp	Leu	Cys	His	Gln	Val	Leu	385	390	395	400
His	His	Cys	Ser	Ser	Ser	Met	Asp	Val	Thr	Arg	Ser	Gln	Ala	Cys	Ala	405	410	415	
Thr	Leu	Tyr	Leu	Leu	Met	Arg	Phe	Ser	Phe	Gly	Ala	Thr	Ser	Asn	Phe	420	425	430	
Ala	Arg	Val	Lys	Met	Gln	Val	Thr	Met	Ser	Leu	Ala	Ser	Leu	Val	Gly	435	440	445	
Arg	Ala	Pro	Asp	Phe	Asn	Glu	Glu	His	Leu	Arg	Arg	Ser	Leu	Arg	Thr	450	455	460	
Ile	Leu	Ala	Tyr	Ser	Glu	Glu	Asp	Thr	Ala	Met	Gln	Met	Thr	Pro	Phe	465	470	475	480
Pro	Thr	Gln	Val	Glu	Glu	Leu	Leu	Cys	Asn	Leu	Asn	Ser	Ile	Leu	Tyr	485	490	495	
Asp	Thr	Val	Lys	Met	Arg	Glu	Phe	Gln	Glu	Asp	Pro	Glu	Met	Leu	Met	500	505	510	
Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Ser	Tyr	Gln	Ala	Ser	Pro	Asp	Leu	515	520	525	
Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Glu	Lys	His	Thr	Lys	Lys	Lys	530	535	540	
Cys	Tyr	Thr	Glu	Ala	Ala	Met	Cys	Leu	Val	His	Ala	Ala	Ala	Leu	Val	545	550	555	560

Val	Ser	Glu	Asp	Thr	Leu	Ser	Pro	Asp	Glu	Asp	Gly	Val	Cys	Ala	Gly		
		595					600					605					
Gln	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	Leu	Leu	Glu	Gln	Ala	Ala		
	610					615					620						
Glu	Leu	Phe	Ser	Thr	Gly	Gly	Leu	Tyr	Glu	Thr	Val	Asn	Glu	Val	Tyr		
625					630					635					640		
Lys	Leu	Val	Ile	Pro	Ile	Leu	Glu	Ala	His	Arg	Glu	Phe	Arg	Lys	Leu		
				645					650					655			
Thr	Leu	Thr	His	Ser	Lys	Leu	Gln	Arg	Ala	Phe	Asp	Ser	Ile	Val	Asn		
			660					665						670			
Lys	Asp	His	Lys	Arg	Met	Phe	Gly	Thr	Tyr	Phe	Arg	Val	Gly	Phe	Phe		
		675					680						685				
Gly	Ser	Lys	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	Lys	Glu		
	690					695						700					
Pro	Ala	Ile	Thr	Lys	Leu	Pro	Glu	Ile	Ser	His	Arg	Leu	Glu	Ala	Phe		
705					710					715					720		
Tyr	Gly	Gln	Cys	Phe	Gly	Ala	Glu	Phe	Val	Glu	Val	Ile	Lys	Asp	Ser		
				725					730					735			
Thr	Pro	Val	Asp	Lys	Thr	Lys	Leu	Asp	Pro	Asn	Lys	Ala	Tyr	Ile	Gln		
			740					745						750			
Ile	Thr	Phe	Val	Glu	Pro	Tyr	Phe	Asp	Glu	Tyr	Glu	Met	Lys	Asp	Arg		
		755					760					765					
Val	Thr	Tyr	Phe	Glu	Lys	Asn	Phe	Asn	Leu	Arg	Arg	Phe	Met	Tyr	Thr		
	770					775					780						
Thr	Pro	Phe	Thr	Leu	Glu	Gly	Arg	Pro	Arg	Gly	Glu	Leu	His	Glu	Gln		
785					790					795					800		
Tyr	Arg	Arg	Asn	Thr	Val	Leu	Thr	Thr	Met	His	Ala	Phe	Pro	Tyr	Ile		
			805						810					815			
Lys	Thr	Arg	Ile	Ser	Val	Ile	Gln	Lys	Glu	Glu	Phe	Val	Leu	Thr	Pro		
			820					825					830				
Ile	Glu	Val	Ala	Ile	Glu	Asp	Met	Lys	Lys	Lys	Thr	Leu	Gln	Leu	Ala		
		835					840						845				
Val	Ala	Ile	Asn	Gln	Glu	Pro	Pro	Asp	Ala	Lys	Met	Leu	Gln	Met	Val		
	850					855					860						
Leu	Gln	Gly	Ser	Val	Gly	Ala	Thr	Val	Asn	Gln	Gly	Pro	Leu	Glu	Val		
865					870					875					880		

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg  
915 920 925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn  
930 935 940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile  
945 950 955 960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe  
965 970 975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser  
980 985

<210> 16

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human CLASP-1

<400> 16

Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Gly  
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro  
20

<210> 17

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human KIAA1058

<400> 17

Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp  
1 5 10 15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu  
20 25 30

Tyr Ile Tyr Lys Glu Pro  
35

<210> 18

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human CLASP-2

<400> 18

Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro  
1 5 10

<210> 19

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human CLASP-6

<400> 19

Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly  
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro  
20

<210> 20

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human CLASP-4

<400> 20

Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly  
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro  
20

<210> 21

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from canonical DOCK180

<400> 21

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly  
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp  
20 25 30

<210> 191

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from canonical DOCK2

<400> 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn  
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp  
20 25 30

<210> 23

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from canonical DOCK3

<400> 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn  
1 5 10 15

Lys Glu Tyr Val Cys Arg Gly His  
20

<210> 24

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human KIAA0716

<400> 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn  
1 5 10 15

Lys Glu Phe Val Cys Arg Gly His  
20

<210> 25

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human CLASP 3

Glu Phe Val Tyr Lys Glu Phe  
20

<210> 26  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motif C  
from rat TRG

<400> 26  
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu  
1 5 10 15  
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser  
20 25 30  
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln  
35 40 45  
Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu  
50 55 60

<210> 27  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-1

<400> 27  
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu  
1 5 10 15  
Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser  
20 25 30  
Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln  
35 40 45  
Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu  
50 55 60

<210> 28  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-2

Tyr Ser Asp Lys Phe Gly Ser Thr Asn Val Lys Met Thr Gln Asp Ser  
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln  
35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu  
50 55 60

<210> 29

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-4

<400> 29

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu  
1 5 10 15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser  
20 25 30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln  
35 40 45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu  
50 55 60

<210> 30

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-3

<400> 30

Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe  
1 5 10 15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser  
20 25 30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln  
35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu  
50 55 60

<210> 31

<223> Description of Artificial Sequence:DOCK motif C  
from human KIAA0716

<400> 31

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu  
1 5 10 15  
Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr  
20 25 30  
Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro  
35 40 45  
Ile Pro Glu Ser Gln Glu  
50

<210> 32

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from canonical DOCK3

<400> 32

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu  
1 5 10 15  
Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala  
20 25 30  
Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro  
35 40 45  
Ile Pro Asp Tyr Val Asp  
50

<210> 33

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from Canonical DOCK2

<400> 33

Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn  
1 5 10 15  
Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr  
20 25 30  
Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro

<210> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from Canonical DOCK180

<400> 34

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe  
1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val  
20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val  
35 40 45

Leu Asp Glu His Pro  
50

<210> 35

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
and E from human CLASP-1

<400> 35

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg  
1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val  
20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn  
35 40 45

<210> 36

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
and E from rat TRG

<400> 36

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
20 25 30

<210> 37  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from human KIAA1058

<400> 37  
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
1 5 10 15  
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
20 25 30  
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg  
35 40 45

<210> 38  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from human CLASP-2

<400> 38  
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
1 5 10 15  
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
20 25 30  
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg  
35 40 45

<210> 39  
<211> 44  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from human CLASP-6

<400> 39  
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
1 5 10 15  
Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val

<210> 40  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from human CLASP-4

<400> 40  
Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg  
1 5 10 15  
Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val  
20 25 30  
Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln  
35 40 45

<210> 41  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from human CLASP-3

<400> 41  
Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg  
1 5 10 15  
Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val  
20 25 30  
Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala  
35 40 45

<210> 42  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from human CLASP-5

<400> 42  
Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg  
1 5 10 15  
Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val

<210> 43

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
and E from human KIAA0716

<400> 43

Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp  
1 5 10 15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn  
20 25 30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys  
35 40 45

<210> 44

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
and E from canonical DOCK2

<400> 44

Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp  
1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn  
20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu  
35 40 45

<210> 45

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
and E from canonical DOCK3

<400> 45

Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp  
1 5 10 15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn

<210> 46  
<211> 45  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs D  
and E from canonical DOCK180

<400> 46  
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp  
1 5 10 15  
Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn  
20 25 30  
Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu  
35 40 45

<210> 47  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-1

<400> 47  
Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala  
1 5 10 15  
Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys  
20 25 30  
Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln  
35 40 45  
Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp  
50 55

<210> 48  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from rat TRG

<400> 48  
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
  
Arg Tyr Phe Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Ile  
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
50 55

<210> 49  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from human KIAA1058

<400> 49  
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
50 55

<210> 50  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-2

<400> 50  
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
50 55

<210> 51  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<400> 51

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
50 55

<210> 52

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-3

<400> 52

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln  
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp  
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp  
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg  
50 55

<210> 53

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP 4

<400> 53

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala  
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser  
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys

<210> 54  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-5

<400> 54

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln  
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp  
20 25 30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu  
35 40 45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu  
50 55

<210> 55  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human KIAA0716

<400> 55

Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly  
1 5 10 15

Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu  
20 25 30

Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met  
35 40 45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala  
50 55 60

<210> 56  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from canonical DOCK2

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Ile Thr Ile Val Tyr Val Arg  
20 25 30

Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile  
35 40 45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys  
50 55 60

<210> 57

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from canonical DOCK3

<400> 57

Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly  
1 5 10 15

Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn  
20 25 30

Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met  
35 40 45

Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala  
50 55 60

<210> 58

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from canonical DOCK180

<400> 58

Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly  
1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg  
20 25 30

Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile  
35 40 45

Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg  
50 55 60

<210> 59

<220>

<223> Description of Artificial Sequence:Ref 1.1  
sequence of bacterial artificial chromosome BAC19  
using primer HC5S11

<220>

<221> modified\_base

<222> (1)..(598)

<223> n = g, a, c or t

<400> 59

```
ctctctgtct tcatatcttc caggttataa agnattatth actaaaagaa nattcanget 60
atttcattta actagctcag tttaatcatg tatttcctat aaagggttagt cttattaatt 120
tgacaaaaca atcaaacaaat tcaaaccaga tcaagtatgc taccctgaag ttacaccact 180
agctaagaat taacaatcta agtaattggt ttctccccag gctcaaggct ccctgatcag 240
gttaagtaaa gccagaatc caataagccc tatgaaatth agaaactcat agaaaagtct 300
caaattcttc tgtctgacat tagccaattg ttatattatg caaatagagg attncaagta 360
aataagtttg gaacctgttt accaggthtt tgcagcagnc ctctaagagc ttaactgggc 420
atgcattgaa tgccgagagc aaagaggaat ggagaggggn tgtaagnggt tccaatntta 480
ctggaaccca ccactatctt tngaagtctt gatacttaac tngtgtagn ctcttttaggc 540
ctntantaan tagaatctat atggattcgt gttctgtcng caagnagtgc ctatgaaa 598
```

<210> 60

<211> 625

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 2.1  
sequence of bacterial artificial chromosome BAC19  
using primer HC5AS10b

<220>

<221> modified\_base

<222> (1)..(625)

<223> n = g, a, c or t

<400> 60

```
tgccgagtagt gtccgcgttc agcatgttgt actgcttata gggctgaagg gaggcacgat 60
tgggggatgg aggccaggga agaagtcaag caacagaaaa atttgaggct taacagtcaa 120
gcaacagaaa aattcaaagt gttctcttaa aataccatga ctgtacatca ctgctaggct 180
ggagatctat tgccagtagc cctgccttcc ctaggcaggg gaagcttgtt tctttgagta 240
gggctactca gcaaagaggg tcacctgggg cagtatttga gctaggcttt cagccaccgt 300
atctgagtag ctctgtctta ngagcagtg gtgctgggtga tcacctctgg gcttgatca 360
tgggtgctgc aatcccagtg atacaaagag gctttcatgc tgctaagatc tccaagtatt 420
tctccttcgt gctgggcagc agagggttag acttncaggg gagaaggaaa ctggctgggt 480
gcatgaata ancttgctgt tcaagantta acttctttgt tacataagng caaagggtata 540
acataaaggg ncatgaactg ctcaacnaaa ttnatcaaat ccatgtttgt gggagttctt 600
ttgtnatngg aagtttaacc cctaa 625
```

<210> 61

<211> 684

<212> DNA  
<213> Artificial Sequence  
sequence of bacterial artificial chromosome BAC19  
using primer C5S3

<220>

<221> modified\_base

<222> (1)..(684)

<223> n = g, a, c or t

<400> 61

```
ccnngctctt tttggcaang taancttggg atgcttggtt tcttctctt aattaagagn 60
aaganttttt tttagcttcat acttctctct tcagggggac caaaagtcac agagcatatt 120
aagtggcana accccnaagg tcttaagtct tcttaggaag aaagcagatg cctgattct 180
gtgggaagcc accatggaga ggaaaagcag tggctcccat atttgaagtg nggacctaac 240
tctagaaagt ttaaaanggc catttgctga agggctatga catgagaaca gagatcaact 300
gagtgaacta gcaanttcac tcttctctctg taanacctct ggtgagtga antaaatcct 360
ntatgtgacg cccattagtc ttacaaaang tcatgccta aaatgccang aaggncagaa 420
atgaatttct caccgccnga ggaatgagga ttatnctggg gggacatgca naaatattnn 480
nccccnatt tattnattta tttatttttg agaengagtn tcnctcta atcgccccagg 540
ctgggnaggtg gnaggtggtt cccatcttna ancttanntn ggaaggncct ctttgngccc 600
cngggggng naaagnga atccctaaatg cctncanncc cctcctgga ngttatttgg 660
gggnntnta aagggcngtg gcng 684
```

<210> 62

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 4.1  
sequence of bacterial artificial chromosome BAC13  
using primer C5S7

<220>

<221> modified\_base

<222> (1)..(450)

<223> n = g, a, c or t

<400> 62

```
acaaaaacta accatcantc tctaaatccc aacaancttt ttttaagaat acctaangag 60
ctcaacnagg gggactntcc aangcactta aatgcagnca aacnacnccn ncaagagnng 120
caactactaa tggggcanat ctnaaagaaa atatagncaa aggnnggaat cataatagga 180
gnaccactt angaagcacc aactggggac ctggaactgn atnaggncct ctacatacat 240
catnnnatan catcctgcaa cgacccttgg aaggaganag anggnattcc tannntagag 300
angaganaac tggggacatg ggaagaggna agcgaagggt tcaaggggan gnaagcgagc 360
agahncaggg gnetcanact ngnggggntt ggggggntnc tgnnncccta cnettnngnan 420
gaacagngnn gttganntgg ctttnganta 450
```

<210> 63

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 5.1  
sequence of bacterial artificial chromosome BAC13

<223> n = g, a, c or t

<400> 63

```
ccannagatt nttgnaacgn nggtaggctt cctttgtaga tttattgaaa atgtttcgta 60
cttctacaag tttgccctgc cttcctataa agagtgaan tcantttgaa tcgactgggtg 120
gataattntt ccatttttcc tcaggcaatt tngagttact ccaataaatt caaatatggg 180
ccagaggaaa tcattcttca gatgggcagt gattggccag tcagcaggag aagctgctta 240
tgccctgttt ggtacattgt ggaaaaaacac actttaataa atacgcantc atgcctgagt 300
acccatcctc catcccgcca cccccagta tggcaaaaat ctggtcagag tccatttggg 360
aataattcca tggttcctgg gatcccaaag cttccagaag tgctggctga tcaanggagt 420
gtacagtcag tcctgggtgg caaaaatgtc ccatttttta agtaccaagc aaaggttcct 480
tcttncaagg gttnttaggg cc 502
```

<210> 64

<211> 202

<212> DNA

<213> Homo sapiens

<220>

<223> 1st partial exon

<400> 64

```
ccagctgcca gccaaagctca gtaaccttcc aacgctcatt tccatgaggc tagagttcct 60
gagaatcctc tgtagccatg agcattacct caatctgaac ctttttttta tgaatgctga 120
tactgtccca acatctcctt gtcttccat atcttcccag gtaataaaag aattatttaa 180
ctaaaagaat tattcaagct at 202
```

<210> 65

<211> 205

<212> DNA

<213> Homo sapiens

<220>

<223> 2nd exon

<400> 65

```
gtcataaaaa tggctcctta cgtttctgta gaactcaagc tcctgtccca gcttccagga 60
ccagaagatc gccagcatgt tcgatctgac ttccgagtao cgccagcagc acttccctcac 120
cgggctcctc ttcacagaac tggctgtgc cctggatgcg gaaggggaag ggtatgtttc 180
tggcatttaa aatggaagat gaagc 205
```

<210> 66

<211> 235

<212> DNA

<213> Homo sapiens

<220>

<223> 3rd exon

<400> 66

```
cataacctct tgattcctgt gttgtgccaa cagaatcagc aaagtacaaa ggaaagctgt 60
cagtgcatt cagagcctgc taagttctca cgacctggac ccacgctgtg tcaaacctaga 120
ggtgaaggtc aaaatcgccg cctttacct acctttagtt ggcattcatt tggatgcttt 180
```

<212> DNA

<213> Homo sapiens

<220>

<223> 4th exon

<400> 67

```
tgtttgactt gacatcacaa acgatgtttt cattgcagtt gcagatactc gcagataaccg 60
caccagtggc tcggatgaag aacaagaagg agccgggtgcc attaaccaga atgtggctct 120
ggccatagca gggaataatt tcaatttgaa aacaagtgga atagtgtctg ctteettggt 180
atgttggtgc acatgtgtct ggttgatttt tcat 214
```

<210> 68

<211> 247

<212> DNA

<213> Homo sapiens

<220>

<223> 5th exon

<400> 68

```
tggcctccat cccccaatct gcttcccttc agccctataa gcagtacaac atgctgaacg 60
cggacactac tcgcaacctc atgatctgct tctcttgat catgaaaaat gctgatcaga 120
gcttcattag gaagtggatt gctgacctgc catcaacgca gctcaacagg attttagatc 180
tacttttcat ctgtgtgtta tgttttgagt ataaggtaag tctggagtgg cacaacttta 240
taccagc 247
```

<210> 69

<211> 205

<212> DNA

<213> Homo sapiens

<220>

<223> 6th exon

<400> 69

```
caccuaagga catgtcctcc tacctctgtc ttgtccaggg aaaacagagt tctgacaaaag 60
tcagtaccca agtcttcag aagtcaaggg atgtcaaggc ccggctggaa gaggccttgc 120
tgcgtgggga aggggccaga ggggagatga tgcgcgcgcg ggctccaggt gtgttggaact 180
ggccttccc tgctctctgt caagc 205
```

<210> 70

<211> 156

<212> DNA

<213> Homo sapiens

<220>

<223> 7th exon

<400> 70

```
tcaaattcct atcatgcatt tcttaactcc tagggaacga ccgatttcca ggccataaatg 60
aaaatttgag atggaagaaa gagcagacac attggcggca agctaagtag aagctagata 120
agtgagtcac tcggcaactt tctgctactt ttacct 156
```

<220>

<223> 8th exon

<400> 71

```
gctttaattt gacctcttgt tgtttcctag aacaaaggcc gagttagatc aagaagcctt 60
gatcagtggc aatctggcta cagaagcaca tttaatcacc ctggatatgc aggaaaacat 120
tatccagggtg aggaaaacaa acaccaatc tgatttg 157
```

<210> 72

<211> 203

<212> DNA

<213> Homo sapiens

<220>

<223> 9th exon

<400> 72

```
ggattcaatg atgctgttct tccattcccc caggcgagct cggtcttga ctgtaaagac 60
agcctgctgg gaggtgttct gaggggtgctg gtgaattctc tgaactgtga tcagagtacc 120
acctacctga ctactgctt tgcaacactc cgtgctctca tcgccaaggt aaacttggga 180
tgcttgtttt ctctctctta att 203
```

<210> 73

<211> 223

<212> DNA

<213> Homo sapiens

<220>

<223> 10th exon

<400> 73

```
agtgatgcct aatggccctt tatgtctctc ctagtgttga gacttactct tcgaagagga 60
ggtggaacag tgtttcgacc tatgtcacca agtcctgcac cactgcagca gcagcatgga 120
tgtcacccgg agccaagcct gtgccacctt ttacctctc atgaggttca gttttggagc 180
caccagtgtg agagttcaaa ccagctgagt gacctggaat cag 223
```

<210> 74

<211> 230

<212> DNA

<213> Homo sapiens

<220>

<223> 11th exon

<400> 74

```
ttacttcacc tttttttttt ttttctactga tgcagaattt tgcaagagta aagatgcaag 60
taaccatgtc cctggcatct ttgggtggga gagcaccaga ctttaatgaa gagcacctga 120
gaagatcctt gaggacaatt ttggcctatt cagaagagga cacagccatg cagatgactc 180
cttttccac ccaggtacac cgaagcacat accttgtctc atgcatgagt 230
```

<220>

<223> 12th exon

<400> 75

```
agctaagatt attttgaggc ttacactttt tgcaggtgga ggaacttctc tgtaatctga 60
atagcatctt atatgacaca gtgaaaatga ggaatttca ggaagatcct gagatgctta 120
tggatctcat gtacaggtaa gctttctctga cacactcaag ggacaccatt t 171
```

<210> 76

<211> 266

<212> DNA

<213> Homo sapiens

<220>

<223> 13th exon

<400> 76

```
tcttcaaaac tactttctcac tcaatctgtc ttcagaattg ccaagagtta ccaggcatct 60
cctgatctgc ggctgacctg gctccagaac atggcagaga aacacaccaa gaagaagtgc 120
tacacggagg ctgccatgtg cctgggtgcac gccgctgcgt tagtggctga gtatctgagc 180
atgctggagg accacagcta cctgcccgtg ggcagtgtca gcttccaggt aggggtgtgtg 240
cagcttttcc cttagagcag tggttc 266
```

<210> 77

<211> 211

<212> DNA

<213> Homo sapiens

<220>

<223> 14th exon

<400> 77

```
ctgtttctcca ggcttatact gtgggtctctt tcagaatatt tcttccaatg tgctggagga 60
gtctgtggtc tctgaggaca cctgtcacc tgacgaggat ggggtgtgct caggccagta 120
cttcaccgag agtggcctgg taggcctcct ggagcaggcc gcggagctct tcagcacggt 180
cagtgcccgag agggcatccc ggggcctggc c 211
```

<210> 78

<211> 199

<212> DNA

<213> Homo sapiens

<220>

<223> 15th exon

<400> 78

```
aattctctct gatgctcttc tctcttttcc aaggagggct tatatgagac agttaatgag 60
gtctacaagc tggtcacccc cctcctagaa gcgcctcgag aattccggaa gctgacactc 120
actcacagca agctgcagag agccttcgac agcatcgta acaaggtagc cggggagcct 180
ggctggcagg tcttggtac 199
```

<210> 79

<211> 208

<400> 79

```
taaggagagc tttttatatt ttgttcctca ggatcataag agaatgtttg gaacctactt 60
ccgagttggt ttctttggat ccaaatttgg ggatttggat gaacaggagt ttgtctacaa 120
agagcctgca attaccaagc ttcttgagat ctccacataga ctagaggtaa gaaaagtgat 180
tctgtgcgcc tgacctggta cactttac                                     208
```

<210> 80

<211> 157

<212> DNA

<213> Homo sapiens

<220>

<223> 17th exon

<400> 80

```
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gaatttgtgg aagtgattaa agactccact cctgtggaca aaaccaagtt ggatcctaac 120
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<210> 87

<211> 2097

<212> DNA

<213> Homo sapiens

<220>

<223> putative human CLASP-5 promoter

<400> 87

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gaggtgtgat	ctcagctcac	tgaacctca	acctcccagg	atcagatgat	tctcctccca	1500
cctcatcctc	ccaagtagcc	gggactacag	gcgcattgcca	ccacacctgg	ctaatttttg	1560
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tacttattac	ttcgaaacca	cttctgcctt	agaaattttg	taaccttccg	ctcagtttcc	1800
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<211> 2008  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human CLASP-4

<400> 88

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Arg	Thr	Val	Gln	Ser	Thr	Val	Pro	Glu	Asp	Ala	Glu	Lys	Arg	Ala	Gln	
			20					25					30			
Ser	Leu	Phe	Val	Lys	Glu	Cys	Ile	Lys	Thr	Tyr	Ser	Thr	Asp	Trp	His	
		35					40					45				
Val	Val	Asn	Tyr	Lys	Tyr	Glu	Asp	Phe	Ser	Gly	Asp	Phe	Arg	Met	Leu	
	50					55					60					
Pro	Cys	Lys	Ser	Leu	Arg	Pro	Glu	Lys	Ile	Pro	Asn	His	Val	Phe	Glu	
65					70					75					80	
Ile	Asp	Glu	Asp	Cys	Glu	Lys	Asp	Glu	Asp	Ser	Ser	Ser	Leu	Cys	Ser	
				85				90						95		
Gln	Lys	Gly	Gly	Val	Ile	Lys	Gln	Gly	Trp	Leu	His	Lys	Ala	Asn	Val	
			100					105					110			
Asn	Ser	Thr	Ile	Thr	Val	Thr	Met	Lys	Val	Phe	Lys	Arg	Arg	Tyr	Phe	
		115					120					125				
Tyr	Leu	Thr	Gln	Leu	Pro	Asp	Gly	Ser	Tyr	Ile	Leu	Asn	Ser	Tyr	Lys	
	130					135					140					
Asp	Glu	Lys	Asn	Ser	Lys	Glu	Ser	Lys	Gly	Cys	Ile	Tyr	Leu	Asp	Ala	
145					150					155				160		
Cys	Ile	Asp	Val	Val	Gln	Cys	Pro	Lys	Met	Arg	Arg	His	Ala	Phe	Glu	
			165						170					175		
Leu	Lys	Met	Leu	Asp	Lys	Tyr	Ser	His	Tyr	Leu	Ala	Ala	Glu	Thr	Glu	
		180						185					190			
Gln	Glu	Met	Glu	Glu	Trp	Leu	Ile	Thr	Leu	Lys	Lys	Ile	Ile	Gln	Ile	
	195					200						205				
Asn	Thr	Asp	Ser	Leu	Val	Gln	Glu	Lys	Lys	Glu	Thr	Val	Glu	Thr	Ala	
	210					215					220					
Gln	Asp	Asp	Glu	Thr	Ser	Ser	Gln	Gly	Lys	Ala	Glu	Asn	Ile	Met	Ala	
225					230					235				240		

Phe Ser Phe Asp Ser Glu Val Gln Arg Leu Asp Phe Ser Gly Ile Glu  
275 280 285

Pro Asp Ile Lys Pro Phe Glu Glu Lys Cys Asn Lys Arg Phe Leu Val  
290 295 300

Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn  
305 310 315 320

Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala  
325 330 335

Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val  
340 345 350

Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr  
355 360 365

Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr  
370 375 380

Ile His Gly Ile Ala Glu Ser Gln Leu Arg Tyr Ile Cln Cln Gly Ile  
385 390 395 400

Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile  
405 410 415

Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile  
420 425 430

Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala  
435 440 445

Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp  
450 455 460

Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp  
465 470 475 480

Gly Arg Phe Ser Pro Leu Tyr Lys Gln Asp Ser Ser Lys Leu Ser Ser  
485 490 495

Glu Asp Ile Leu Lys Leu Leu Ser Glu Tyr Lys Lys Pro Glu Lys Thr  
500 505 510

Lys Leu Gln Ile Ile Pro Gly Gln Leu Asn Ile Thr Val Glu Cys Val  
515 520 525

Pro Val Asp Leu Ser Asn Cys Ile Thr Ser Ser Tyr Val Pro Leu Lys  
530 535 540

Pro Phe Glu Lys Asn Cys Gln Asn Ile Thr Val Glu Val Glu Glu Phe  
545 550 555 560

Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Val	Cys	Val	Glu	Phe	Arg	Asp	Ser	595	600	605
Asp	Glu	Ser	Asp	Ala	Ser	Ala	Leu	Lys	Cys	Ile	Tyr	Gly	Lys	Pro	Ala	610	615	620
Gly	Ser	Val	Phe	Thr	Thr	Asn	Ala	Tyr	Ala	Val	Val	Ser	His	His	Asn	625	630	635
Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Ile	His	645	650	655
Leu	His	Gln	Lys	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys	660	665	670
Glu	Ile	Asn	Thr	Lys	Gly	Thr	Thr	Lys	Lys	Gln	Asp	Thr	Val	Glu	Thr	675	680	685
Pro	Val	Gly	Phe	Ala	Trp	Val	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Ile	Ile	690	695	700
Thr	Phe	Glu	Gln	Gln	Leu	Pro	Val	Ser	Ala	Asn	Leu	Pro	Pro	Gly	Tyr	705	710	715
Leu	Asn	Leu	Asn	Asp	Ala	Glu	Ser	Arg	Arg	Gln	Cys	Asn	Val	Asp	Ile	725	730	735
Lys	Trp	Val	Asp	Gly	Ala	Lys	Pro	Leu	Leu	Lys	Phe	Lys	Ser	His	Leu	740	745	750
Glu	Ser	Thr	Ile	Tyr	Thr	Gln	Asp	Leu	His	Val	His	Lys	Phe	Phe	His	755	760	765
His	Cys	Gln	Leu	Ile	Gln	Ser	Gly	Ser	Lys	Glu	Val	Pro	Gly	Glu	Leu	770	775	780
Ile	Lys	Tyr	Leu	Lys	Cys	Leu	His	Ala	Met	Glu	Ile	Gln	Val	Met	Ile	785	790	795
Gln	Phe	Leu	Pro	Val	Ile	Leu	Met	Gln	Leu	Phe	Arg	Val	Leu	Thr	Asn	805	810	815
Met	Thr	His	Glu	Asp	Asp	Val	Pro	Ile	Asn	Cys	Thr	Met	Val	Leu	Leu	820	825	830
His	Ile	Val	Ser	Lys	Cys	His	Glu	Glu	Gly	Leu	Asp	Ser	Tyr	Leu	Arg	835	840	845
Ser	Phe	Ile	Lys	Tyr	Ser	Phe	Arg	Pro	Glu	Lys	Pro	Ser	Ala	Pro	Gln	850	855	860
Ala	Gln	Leu	Ile	His	Glu	Thr	Leu	Ala	Thr	Thr	Met	Ile	Ala	Ile	Leu	865	870	875

Glu	Glu	Asn	Lys	Ile	Lys	Leu	Pro	Arg	Gly	Gln	Arg	Phe	Pro	Glu	Thr	915	920	925
Tyr	His	His	Val	Leu	His	Ser	Leu	Leu	Leu	Ala	Ile	Ile	Pro	His	Val	930	935	940
Thr	Ile	Arg	Tyr	Ala	Glu	Ile	Pro	Asp	Glu	Ser	Arg	Asn	Val	Asn	Tyr	945	950	955
Ser	Leu	Ala	Ser	Phe	Leu	Lys	Arg	Cys	Leu	Thr	Leu	Met	Asp	Arg	Gly	965	970	975
Phe	Ile	Phe	Asn	Leu	Ile	Asn	Asp	Tyr	Ile	Ser	Gly	Phe	Ser	Pro	Lys	980	985	990
Asp	Pro	Lys	Val	Leu	Ala	Glu	Tyr	Lys	Phe	Glu	Phe	Leu	Gln	Thr	Ile	995	1000	1005
Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	Met	Ala	Phe	Ala	1010	1015	1020
Lys	Pro	Lys	Leu	Gln	Arg	Val	Gln	Asp	Ser	Asn	Leu	Glu	Tyr	Ser	Leu	1025	1030	1035
Ser	Asp	Glu	Tyr	Cys	Lys	His	His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	1045	1050	1055
Glu	Thr	Ser	Ile	Ala	Leu	Gln	Asp	Asn	Tyr	Glu	Ile	Arg	Tyr	Thr	Ala	1060	1065	1070
Ile	Ser	Val	Ile	Lys	Asn	Leu	Leu	Ile	Lys	His	Ala	Phe	Asp	Thr	Arg	1075	1080	1085
Tyr	Gln	His	Lys	Asn	Gln	Gln	Ala	Lys	Ile	Ala	Gln	Leu	Tyr	Leu	Pro	1090	1095	1100
Phe	Val	Gly	Leu	Leu	Leu	Glu	Asn	Ile	Gln	Arg	Leu	Ala	Gly	Arg	Asp	1105	1110	1115
Thr	Leu	Tyr	Ser	Cys	Ala	Ala	Met	Pro	Asn	Ser	Ala	Ser	Arg	Asp	Glu	1125	1130	1135
Phe	Pro	Cys	Gly	Phe	Thr	Ser	Pro	Ala	Asn	Arg	Gly	Ser	Leu	Ser	Thr	1140	1145	1150
Asp	Lys	Asp	Thr	Ala	Tyr	Gly	Ser	Phe	Gln	Asn	Gly	His	Gly	Ile	Lys	1155	1160	1165
Arg	Glu	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Pro	Glu	Gly	Ala	Thr	Gly	Phe	1170	1175	1180
Pro	Asp	Gln	Gly	Asn	Thr	Gly	Glu	Asn	Thr	Arg	Gln	Ser	Ser	Thr	Arg	1185	1190	1195

Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile  
 1235 1240 1245

Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys  
 1250 1255 1260

Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly  
 1265 1270 1275 1280

Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly  
 1285 1290 1295

Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe  
 1300 1305 1310

Thr Leu Asn His Ser Ser Thr Thr Thr Glu Ala Asp Ile Phe His Gln  
 1315 1320 1325

Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu  
 1330 1335 1340

Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn  
 1345 1350 1355 1360

Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu  
 1365 1370 1375

Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe  
 1380 1385 1390

Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys  
 1395 1400 1405

Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys  
 1410 1415 1420

Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu  
 1425 1430 1435 1440

Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe  
 1445 1450 1455

Leu Arg Thr His Leu Gln Ile Ile Ile Ala Val Ser Gln Leu Ile Ala  
 1460 1465 1470

Asp Val Ala Leu Ser Gly Gly Ser Arg Phe Gln Glu Ser Leu Phe Ile  
 1475 1480 1485

Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro Met Lys Ala Thr Ala Phe  
 1490 1495 1500

Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met  
 1505 1510 1515 1520

Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly	1555	1560	1565
Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val	1570	1575	1580
Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala	1585	1590	1595 1600
Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu	1605	1610	1615
Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu	1620	1625	1630
Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu	1635	1640	1645
Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg	1650	1655	1660
Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala	1665	1670	1675 1680
Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly	1685	1690	1695
Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu	1700	1705	1710
Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser	1715	1720	1725
Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr	1730	1735	1740
Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu	1745	1750	1755 1760
Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr	1765	1770	1775
Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn	1780	1785	1790
His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly	1795	1800	1805
Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu	1810	1815	1820
Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn	1825	1830	1835 1840

Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val  
1875 1880 1885

Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp  
1890 1895 1900

Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp  
1905 1910 1915 1920

Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn  
1925 1930 1935

Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys  
1940 1945 1950

Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu  
1955 1960 1965

Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr  
1970 1975 1980

Leu His val Phe Cys Ala ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr  
1985 1990 1995 2000

Gly Ser Pro Arg Tyr Ala Glu Val  
2005

<210> 89

<211> 2015

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-5

<400> 89

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Asp Phe Thr Asp Asp Asp Leu Asp Val Val Phe Thr Pro Lys Glu Cys  
20 25 30

Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro  
35 40 45

His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val  
50 55 60

Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr  
65 70 75 80

Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu  
85 90 95

Cys	Asp	Phe	Asp	Leu	Arg	Ser	Leu	Gln	Pro	Asp	Lys	Arg	Leu	Glu	Asn
130						135					140				
Leu	Leu	Gln	Gln	Val	Ser	Ala	Glu	Asp	Phe	Glu	Lys	Gln	Asn	Glu	Glu
145					150					155					160
Ala	Arg	Arg	Thr	Asn	Arg	Gln	Ala	Glu	Leu	Phe	Ala	Leu	Tyr	Pro	Ser
				165					170					175	
Val	Asp	Glu	Glu	Asp	Ala	Val	Glu	Ile	Arg	Pro	Val	Pro	Glu	Cys	Pro
			180					185					190		
Lys	Glu	His	Leu	Gly	Asn	Arg	Ile	Leu	Val	Lys	Leu	Leu	Thr	Leu	Lys
		195					200					205			
Phe	Glu	Ile	Glu	Ile	Glu	Pro	Leu	Phe	Ala	Ser	Ile	Ala	Leu	Tyr	Asp
	210					215					220				
Val	Lys	Glu	Arg	Lys	Lys	Ile	Ser	Glu	Asn	Phe	His	Cys	Asp	Leu	Asn
225					230					235					240
Ser	Asp	Gln	Phe	Lys	Gly	Phe	Leu	Arg	Ala	His	Thr	Pro	Ser	Val	Ala
				245					250					255	
Ala	Ser	Ser	Gln	Ala	Arg	Ser	Ala	Val	Phe	Ser	Val	Thr	Tyr	Pro	Ser
			260					265					270		
Ser	Asp	Ile	Tyr	Leu	Val	Val	Lys	Ile	Glu	Lys	Val	Leu	Gln	Gln	Gly
		275					280					285			
Asp	Ile	Gly	Asp	Cys	Ala	Glu	Pro	Tyr	Thr	Val	Ile	Lys	Glu	Ser	Asp
	290					295					300				
Gly	Gly	Lys	Ser	Lys	Glu	Lys	Ile	Glu	Lys	Leu	Lys	Leu	Gln	Ala	Glu
305					310					315					320
Ser	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala
				325					330					335	
Pro	Ile	Ser	Leu	Ser	Ser	Phe	Phe	Asn	Val	Ser	Thr	Leu	Glu	Arg	Glu
			340					345					350		
Val	Thr	Asp	Val	Asp	Ser	Val	Val	Gly	Arg	Ser	Pro	Val	Gly	Glu	Arg
		355						360				365			
Arg	Thr	Leu	Ala	Gln	Ser	Arg	Arg	Leu	Ser	Glu	Arg	Ala	Leu	Ser	Leu
	370					375					380				
Glu	Glu	Asn	Gly	Val	Gly	Ser	Asn	Phe	Lys	Thr	Ser	Thr	Leu	Ser	Val
385					390					395					400
Ser	Ser	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu
				405					410					415	

Glu	Ile	Ile	Asn	Cys	Cys	Leu	Thr	Pro	Glu	Met	Leu	Pro	Val	Lys	Pro	450	455	460
Phe	Pro	Glu	Asn	Arg	Thr	Arg	Pro	His	Lys	Glu	Ile	Leu	Glu	Phe	Pro	465	470	475 480
Thr	Arg	Glu	Val	Tyr	Val	Pro	His	Thr	Val	Tyr	Arg	Asn	Leu	Leu	Tyr	485	490	495
Val	Tyr	Pro	Gln	Arg	Leu	Asn	Phe	Val	Asn	Lys	Leu	Ala	Ser	Ala	Arg	500	505	510
Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn	515	520	525
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln	530	535	540
Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr	545	550	555 560
Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His	565	570	575
Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala	580	585	590
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn	595	600	605
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys	610	615	620
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln	625	630	635 640
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile	645	650	655
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu	660	665	670
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro	675	680	685
Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu	690	695	700
Leu	Lys	Leu	Ser	Ile	Ile	Cys	Leu	Asn	Ser	Ser	Arg	Leu	Glu	Pro	Leu	705	710	715 720
Val	Leu	Phe	Leu	His	Leu	Val	Leu	Asp	Lys	Leu	Phe	Gln	Leu	Ser	Val	725	730	735

Leu	Ser	Lys	Asp	Gln	His	Gly	Arg	Asn	Cys	Leu	Leu	Ala	Ser	Tyr	Val	770	775	780
His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser	785	790	795
Gly	Ala	Pro	Thr	Ala	Leu	Leu	Asp	Pro	Arg	Ser	Tyr	His	Thr	Tyr	Gly	805	810	815
Arg	Thr	Ser	Ala	Ala	Ala	Val	Ser	Ser	Lys	Leu	Leu	Gln	Ala	Arg	Val	820	825	830
Met	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Gly	Thr	His	Ser	Ala	Ala	Asp	835	840	845
Glu	Glu	Val	Lys	Asn	Ile	Met	Ser	Ser	Lys	Ile	Ala	Asp	Arg	Asn	Cys	850	855	860
Ser	Arg	Met	Ser	Tyr	Tyr	Cys	Ser	Gly	Ser	Ser	Asp	Ala	Pro	Ser	Ser	865	870	875
Pro	Ala	Ala	Pro	Arg	Pro	Ala	Ser	Lys	Lys	His	Phe	His	Glu	Glu	Leu	885	890	895
Ala	Leu	Gln	Met	Val	Val	Ser	Thr	Gly	Met	Val	Lys	Ser	Met	Ala	Gln	900	905	910
His	Val	His	Asn	Met	Asp	Lys	Arg	Asp	Ser	Phe	Arg	Arg	Thr	Arg	Phe	915	920	925
Ser	Asp	Arg	Phe	Met	Asp	Asp	Ile	Thr	Thr	Ile	Val	Asn	Val	Val	Thr	930	935	940
Ser	Glu	Ile	Ala	Ala	Leu	Leu	Val	Lys	Pro	Gln	Lys	Glu	Asn	Glu	Gln	945	950	955
Ala	Glu	Lys	Met	Asn	Ile	Ser	Leu	Ala	Phe	Phe	Leu	Tyr	Asp	Leu	Leu	965	970	975
Ser	Leu	Met	Asp	Arg	Gly	Phe	Val	Phe	Asn	Leu	Ile	Arg	His	Tyr	Cys	980	985	990
Ser	Gln	Leu	Ser	Ala	Lys	Leu	Ser	Asn	Leu	Pro	Thr	Leu	Ile	Ser	Met	995	1000	1005
Arg	Leu	Glu	Phe	Leu	Arg	Ile	Leu	Cys	Ser	His	Glu	His	Tyr	Leu	Asn	1010	1015	1020
Leu	Asn	Leu	Phe	Phe	Met	Asn	Ala	Asp	Thr	Ala	Pro	Thr	Ser	Pro	Cys	1025	1030	1035
Pro	Ser	Ile	Ser	Ser	Gln	Asn	Ser	Ser	Ser	Cys	Ser	Ser	Phe	Gln	Asp	1045	1050	1055

Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala  
 1090 1095 1100

Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys  
 1105 1110 1115 1120

Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly  
 1125 1130 1135

Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp  
 1140 1145 1150

Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala  
 1155 1160 1165

Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe  
 1170 1175 1180

Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln  
 1185 1190 1195 1200

Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe  
 1205 1210 1215

Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile  
 1220 1225 1230

Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe  
 1235 1240 1245

Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys  
 1250 1255 1260

Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu  
 1265 1270 1275 1280

Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg  
 1285 1290 1295

Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu  
 1300 1305 1310

Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu  
 1315 1320 1325

Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn  
 1330 1335 1340

Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile  
 1345 1350 1355 1360

Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly  
 1365 1370 1375

Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys			
1410	1415	1420	
His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser			
1425	1430	1435	1440
Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala			
1445	1450	1455	
Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala			
1460	1465	1470	
Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg			
1475	1480	1485	
Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln			
1490	1495	1500	
Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Cys Asn Leu Asn			
1505	1510	1515	1520
Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro			
1525	1530	1535	
Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala			
1540	1545	1550	
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His			
1555	1560	1565	
Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala			
1570	1575	1580	
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr			
1585	1590	1595	1600
Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu			
1605	1610	1615	
Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly			
1620	1625	1630	
Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu			
1635	1640	1645	
Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val			
1650	1655	1660	
Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu			
1665	1670	1675	1680
Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp			
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[illegible]

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<223> human CLASP-3

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Ala	Glu	Val	Arg	Lys	Gln	Ile	Ser	Gly	Gln	Tyr	Ser	Gly	Ser	Pro	Gln	
			20					25					30			
Leu	Leu	Lys	Asn	Leu	Asn	Ile	Val	Gly	Asn	Ile	Ser	His	His	Thr	Thr	
		35					40					45				
Val	Pro	Leu	Thr	Glu	Ala	Val	Asp	Pro	Val	Asp	Leu	Glu	Asp	Tyr	Leu	
	50					55					60					
Ile	Thr	His	Pro	Leu	Ala	Val	Asp	Ser	Gly	Pro	Leu	Arg	Asp	Leu	Ile	
65					70					75					80	
Glu	Phe	Pro	Pro	Asp	Asp	Ile	Glu	Val	Val	Tyr	Ser	Pro	Arg	Asp	Cys	
				85					90					95		
Arg	Thr	Leu	Val	Ser	Ala	Val	Pro	Glu	Glu	Ser	Glu	Met	Asp	Pro	His	
		100						105					110			
Val	Arg	Asp	Cys	Ile	Arg	Ser	Tyr	Thr	Glu	Asp	Trp	Ala	Ile	Val	Ile	
		115					120					125				
Arg	Lys	Tyr	His	Lys	Leu	Gly	Thr	Gly	Phe	Asn	Pro	Asn	Thr	Leu	Asp	
	130					135					140					
Lys	Gln	Lys	Glu	Arg	Gln	Lys	Gly	Leu	Pro	Lys	Gln	Val	Phe	Glu	Ser	
145					150					155					160	
Asp	Glu	Ala	Pro	Asp	Gly	Asn	Ser	Tyr	Gln	Asp	Asp	Gln	Asp	Asp	Leu	
				165					170					175		
Lys	Arg	Arg	Ser	Met	Ser	Ile	Asp	Asp	Thr	Pro	Arg	Gly	Ser	Trp	Ala	
			180					185					190			
Cys	Ser	Ile	Phe	Asp	Leu	Lys	Asn	Ser	Leu	Pro	Asp	Ala	Leu	Leu	Pro	
		195					200					205				
Asn	Leu	Leu	Asp	Arg	Thr	Pro	Asn	Glu	Glu	Ile	Asp	Arg	Gln	Asn	Asp	
	210					215					220					
Asp	Gln	Arg	Lys	Ser	Asn	Arg	His	Lys	Glu	Leu	Phe	Ala	Leu	His	Pro	
225					230					235					240	
Ser	Pro	Asp	Glu	Glu	Glu	Pro	Ile	Glu	Arg	Leu	Ser	Val	Pro	Asp	Ile	
			245						250					255		
Pro	Lys	Glu	His	Phe	Gly	Gln	Arg	Leu	Leu	Val	Lys	Cys	Leu	Ser	Leu	
			260				265						270			
Asp	Val	Lys	Leu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	
	280					285							290			

Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	Pro	His	Val	Pro	Pro	Ala
305					310					315					320
Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Ile	Thr	Tyr	Pro
				325					330					335	
Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln
			340					345					350		
Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	Met	Ile	Phe	Lys	Glu	Ala
		355					360					365			
Asp	Ala	Thr	Lys	Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Lys	Ser	Gln	Ala
		370				375					380				
Asp	Gln	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp
385					390					395					400
Thr	Ala	Ile	His	Leu	Met	Asn	Ile	Val	Ser	Ser	Ala	Gly	Ser	Leu	Glu
				405					410					415	
Arg	Asp	Ser	Thr	Glu	Val	Glu	Ile	Ser	Thr	Gly	Glu	Arg	Lys	Gly	Ser
			420					425					430		
Trp	Ser	Glu	Arg	Arg	Asn	Ser	Ser	Ile	Val	Gly	Arg	Arg	Ser	Leu	Glu
		435					440					445			
Arg	Thr	Thr	Ser	Gly	Asp	Asp	Ala	Cys	Asn	Leu	Thr	Ser	Phe	Arg	Pro
		450				455					460				
Ala	Thr	Leu	Thr	Val	Thr	Asn	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu
465					470					475					480
Ser	Asp	Glu	Asp	Leu	Tyr	Lys	Phe	Leu	Ala	Asp	Met	Arg	Arg	Pro	Ser
				485					490					495	
Ser	Val	Leu	Arg	Arg	Leu	Arg	Pro	Ile	Thr	Ala	Gln	Leu	Lys	Ile	Asp
			500					505					510		
Ile	Ser	Pro	Ala	Pro	Glu	Asn	Pro	His	Tyr	Cys	Leu	Thr	Pro	Glu	Leu
		515					520					525			
Leu	Gln	Val	Lys	Leu	Tyr	Pro	Asp	Ser	Arg	Val	Arg	Pro	Thr	Arg	Glu
		530				535					540				
Ile	Leu	Glu	Phe	Pro	Ala	Arg	Asp	Val	Tyr	Val	Pro	Asn	Thr	Thr	Tyr
545					550					555					560
Arg	Asn	Leu	Leu	Tyr	Ile	Tyr	Pro	Gln	Ser	Leu	Asn	Phe	Ala	Asn	Arg
				565					570					575	
Gln	Gly	Ser	Ala	Arg	Asn	Ile	Thr	Val	Lys	Val	Gln	Phe	Met	Tyr	Gly
			580					585					590		

Ser	Pro	Asp	Phe	His	Glu	Glu	Ile	Lys	Val	Lys	Leu	Pro	Ala	Thr	Leu	625	630	635	640
Thr	Asp	His	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys	Gln	645	650	655	
Gln	Lys	Gln	Asn	Thr	Pro	Leu	Glu	Thr	Pro	Val	Gly	Tyr	Thr	Trp	Ile	660	665	670	
Pro	Met	Leu	Gln	Asn	Gly	Arg	Leu	Lys	Thr	Gly	Gln	Phe	Cys	Leu	Pro	675	680	685	
Val	Ser	Leu	Glu	Lys	Pro	Pro	Gln	Ala	Tyr	Ser	Val	Leu	Ser	Pro	Glu	690	695	700	
Val	Pro	Leu	Pro	Gly	Met	Lys	Trp	Val	Asp	Asn	His	Lys	Gly	Val	Phe	705	710	715	720
Asn	Val	Glu	Val	Val	Ala	Val	Ser	Ser	Ile	His	Thr	Gln	Asp	Pro	Tyr	725	730	735	
Leu	Asp	Lys	Phe	Phe	Ala	Leu	Val	Asn	Ala	Leu	Asp	Glu	His	Leu	Phe	740	745	750	
Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	Glu	Asn	Asn	Leu	Glu	Asn	755	760	765	
Glu	Leu	Lys	Ser	Ser	Ile	Ser	Ala	Leu	Asn	Ser	Ser	Gln	Leu	Glu	Pro	770	775	780	
Val	Val	Arg	Phe	Leu	His	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Leu	Leu	Val	785	790	795	800
Ile	Arg	Pro	Pro	Val	Ile	Ala	Gly	Gln	Ile	Val	Asn	Leu	Gly	Gln	Ala	805	810	815	
Ser	Phe	Glu	Ala	Met	Ala	Ser	Ile	Ile	Asn	Arg	Leu	His	Lys	Asn	Leu	820	825	830	
Glu	Gly	Asn	His	Asp	Gln	His	Gly	Arg	Asn	Ser	Leu	Leu	Ala	Ser	Tyr	835	840	845	
Ile	His	Tyr	Val	Phe	Arg	Leu	Pro	Asn	Thr	Tyr	Pro	Asn	Ser	Ser	Ser	850	855	860	
Pro	Gly	Pro	Gly	Gly	Leu	Gly	Gly	Ser	Val	His	Tyr	Ala	Thr	Met	Ala	865	870	875	880
Arg	Ser	Ala	Val	Arg	Pro	Ala	Ser	Leu	Asn	Leu	Asn	Arg	Ser	Arg	Ser	885	890	895	
Leu	Ser	Asn	Ser	Asn	Pro	Asp	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Pro	Asp	900	905	910	

Pro	Ser	Pro	Ser	Ala	Glu	Ser	Thr	Gln	Ala	Met	Asp	Arg	Ser	Cys	Asn	945	950	955	960
Arg	Met	Ser	Ser	His	Thr	Glu	Thr	Ser	Ser	Phe	Leu	Gln	Thr	Leu	Thr	965	970	975	
Gly	Arg	Leu	Pro	Thr	Lys	Lys	Leu	Phe	His	Glu	Glu	Leu	Ala	Leu	Gln	980	985	990	
Trp	Val	Val	Cys	Ser	Gly	Ser	Val	Arg	Glu	Ser	Ala	Leu	Gln	Gln	Ala	995	1000	1005	
Trp	Phe	Phe	Phe	Glu	Leu	Met	Val	Lys	Ser	Met	Val	His	His	Leu	Tyr	1010	1015	1020	
Phe	Asn	Asp	Lys	Leu	Glu	Ala	Pro	Arg	Lys	Ser	Arg	Phe	Pro	Glu	Arg	1025	1030	1035	1040
Phe	Met	Asp	Asp	Ile	Ala	Ala	Leu	Val	Ser	Thr	Ile	Ala	Ser	Asp	Ile	1045	1050	1055	
Val	Ser	Arg	Phe	Gln	Lys	Asp	Thr	Glu	Met	Val	Glu	Arg	Leu	Asn	Thr	1060	1065	1070	
Ser	Leu	Ala	Phe	Phe	Leu	Asn	Asp	Leu	Leu	Ser	Val	Met	Asp	Arg	Gly	1075	1080	1085	
Phe	Val	Phe	Ser	Leu	Ile	Lys	Ser	Cys	Tyr	Lys	Gln	Val	Ser	Ser	Lys	1090	1095	1100	
Leu	Tyr	Ser	Leu	Pro	Asn	Pro	Ser	Val	Leu	Val	Ser	Leu	Arg	Leu	Asp	1105	1110	1115	1120
Phe	Leu	Arg	Ile	Ile	Cys	Ser	His	Glu	His	Tyr	Val	Thr	Leu	Asn	Leu	1125	1130	1135	
Pro	Cys	Ser	Leu	Leu	Thr	Pro	Pro	Ala	Ser	Pro	Ser	Pro	Ser	Val	Ser	1140	1145	1150	
Ser	Ala	Thr	Ser	Gln	Ser	Ser	Gly	Phe	Ser	Thr	Asn	Val	Gln	Asp	Gln	1155	1160	1165	
Lys	Ile	Ala	Asn	Met	Phe	Glu	Leu	Ser	Val	Pro	Phe	Arg	Gln	Gln	His	1170	1175	1180	
Tyr	Leu	Ala	Gly	Leu	Val	Leu	Thr	Glu	Leu	Ala	Val	Ile	Leu	Asp	Pro	1185	1190	1195	1200
Asp	Ala	Glu	Gly	Leu	Phe	Gly	Leu	His	Lys	Lys	Val	Ile	Asn	Met	Val	1205	1210	1215	
His	Asn	Leu	Leu	Ser	Ser	His	Asp	Ser	Asp	Pro	Arg	Tyr	Ser	Asp	Pro	1220	1225	1230	

Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu			
1265	1270	1275	1280
Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr			
1285	1290	1295	
Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr			
1300	1305	1310	
Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu			
1315	1320	1325	
Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu			
1330	1335	1340	
Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu			
1345	1350	1355	1360
Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys			
1365	1370	1375	
Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met			
1380	1385	1390	
Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln			
1395	1400	1405	
Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly			
1410	1415	1420	
Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr			
1425	1430	1435	1440
His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile			
1445	1450	1455	
Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu			
1460	1465	1470	
Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr			
1475	1480	1485	
Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His			
1490	1495	1500	
Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala			
1505	1510	1515	1520
Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu			
1525	1530	1535	
Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys			
1540	1545	1550	

Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln  
 1585 1590 1595 1600  
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr  
 1605 1610 1615  
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln  
 1620 1625 1630  
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val  
 1635 1640 1645  
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met  
 1650 1655 1660  
 Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp  
 1665 1670 1675 1680  
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu  
 1685 1690 1695  
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu  
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 Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe  
 1715 1720 1725  
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp  
 1730 1735 1740  
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr  
 1745 1750 1755 1760  
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser  
 1765 1770 1775  
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile  
 1780 1785 1790  
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His  
 1795 1800 1805  
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly  
 1810 1815 1820  
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr  
 1825 1830 1835 1840  
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala  
 1845 1850 1855  
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly  
 1860 1865 1870

Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr  
1905 1910 1915 1920

Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro  
1925 1930 1935

Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys  
1940 1945 1950

Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr  
1955 1960 1965

Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu  
1970 1975 1980

Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala  
1985 1990 1995 2000

Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln  
2005 2010 2015

Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln  
2020 2025 2030

Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His  
2035 2040 2045

Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp  
2050 2055 2060

Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr  
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Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro  
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<212> PRT

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Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu  
20 25 30

Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp  
35 40 45

... ..  
... ..

Tyr	Glu	Val	Asp	Glu	Glu	Val	Asp	Lys	Asp	Glu	Asp	Ala	Ala	Ser	Leu	85	90	95
Gly	Ser	Gln	Lys	Gly	Gly	Ile	Thr	Lys	His	Gly	Trp	Leu	Tyr	Lys	Gly	100	105	110
Asn	Met	Asn	Ser	Ala	Ile	Ser	Val	Thr	Met	Arg	Ser	Phe	Lys	Arg	Arg	115	120	125
Phe	Phe	His	Leu	Ile	Gln	Leu	Gly	Asp	Gly	Ser	Tyr	Asn	Leu	Asn	Phe	130	135	140
Tyr	Lys	Asp	Glu	Lys	Ile	Ser	Lys	Glu	Pro	Lys	Gly	Ser	Ile	Phe	Leu	145	150	155
Asp	Ser	Cys	Met	Gly	Val	Val	Gln	Asn	Asn	Lys	Val	Arg	Arg	Phe	Ala	165	170	175
Phe	Glu	Leu	Lys	Met	Gln	Asp	Lys	Ser	Ser	Tyr	Leu	Leu	Ala	Ala	Asp	180	185	190
Ser	Glu	Val	Glu	Met	Glu	Glu	Trp	Ile	Thr	Ile	Leu	Asn	Lys	Ile	Leu	195	200	205
Gln	Leu	Asn	Phe	Glu	Ala	Ala	Met	Gln	Glu	Lys	Arg	Asn	Gly	Asp	Ser	210	215	220
His	Glu	Asp	Asp	Glu	Gln	Ser	Lys	Leu	Glu	Gly	Ser	Gly	Ser	Gly	Leu	225	230	235
Asp	Ser	Tyr	Leu	Pro	Glu	Leu	Ala	Lys	Ser	Ala	Arg	Glu	Ala	Glu	Ile	245	250	255
Lys	Leu	Lys	Ser	Glu	Ser	Arg	Val	Lys	Leu	Phe	Tyr	Leu	Asp	Pro	Asp	260	265	270
Ala	Gln	Lys	Leu	Asp	Phe	Ser	Ser	Ala	Glu	Pro	Glu	Val	Lys	Ser	Phe	275	280	285
Glu	Glu	Lys	Phe	Gly	Lys	Arg	Ile	Leu	Val	Lys	Cys	Asn	Asp	Leu	Ser	290	295	300
Phe	Asn	Leu	Gln	Cys	Cys	Val	Ala	Glu	Asn	Glu	Gly	Pro	Thr	Thr		305	310	315
Asn	Val	Glu	Pro	Phe	Phe	Val	Thr	Leu	Ser	Leu	Phe	Asp	Ile	Lys	Tyr	325	330	335
Asn	Arg	Lys	Ile	Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Phe	Ser	340	345	350
Val	Arg	Gln	Met	Leu	Ala	Thr	Thr	Ser	Pro	Ala	Leu	Met	Asn	Gly	Ser	355	360	365

Ile	Phe	Leu	Val	Ala	Arg	Ile	Glu	Lys	Val	Leu	Gln	Gly	Ser	Ile	Thr	405	410	415
His	Cys	Ala	Glu	Pro	Tyr	Met	Lys	Ser	Ser	Asp	Ser	Ser	Lys	Val	Ala	420	425	430
Gln	Lys	Val	Leu	Lys	Asn	Ala	Lys	Gln	Ala	Cys	Gln	Arg	Leu	Gly	Gln	435	440	445
Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	Ala	Arg	Thr	Leu	Phe	Lys	Asp	Ala	450	455	460
Ser	Gly	Asn	Leu	Asp	Lys	Asn	Ala	Arg	Phe	Ser	Ala	Ile	Tyr	Arg	Gln	465	470	475
Asp	Ser	Asn	Lys	Leu	Ser	Asn	Asp	Asp	Met	Leu	Lys	Leu	Leu	Ala	Asp	485	490	495
Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly	Asn	500	505	510
Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr	Val	515	520	525
Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr	530	535	540
Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His	545	550	555
Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys	565	570	575
Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile	580	585	590
Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro	595	600	605
Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser	610	615	620
Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	625	630	635
Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	645	650	655
Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	660	665	670
Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	675	680	685

Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	725	730	735
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	740	745	750
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	755	760	765
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	770	775	780
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	785	790	795
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	805	810	815
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	820	825	830
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	835	840	845
Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	850	855	860
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	865	870	875
Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	885	890	895
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	900	905	910
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	915	920	925
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	930	935	940
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	945	950	955
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	965	970	975
Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	980	985	990
Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	995	1000	1005

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 Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu  
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 1075 1080 1085  
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 Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro  
 1125 1130 1135  
 Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys  
 1140 1145 1150  
 Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser  
 1155 1160 1165  
 Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu  
 1170 1175 1180  
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys  
 1185 1190 1195 1200  
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser  
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 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu  
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Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His  
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 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val  
 1505 1510 1515 1520  
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln  
 1525 1530 1535  
 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr  
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 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp  
 1555 1560 1565  
 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu  
 1570 1575 1580  
 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu  
 1585 1590 1595 1600  
 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile  
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 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met  
 1620 1625 1630  
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln  
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Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr  
 1685 1690 1695

Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys  
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Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn  
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Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val  
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Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe  
 1745 1750 1755 1760

Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr  
 1765 1770 1775

Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg  
 1780 1785 1790

Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile  
 1795 1800 1805

Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala  
 1810 1815 1820

Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser  
 1825 1830 1835 1840

Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser  
 1845 1850 1855

Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe  
 1860 1865 1870

Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu  
 1875 1880 1885

Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu  
 1890 1895 1900

Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu  
 1905 1910 1915 1920

Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile  
 1925 1930 1935

Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro  
 1940 1945 1950

Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr  
 1955 1960 1965

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<211> 2045

<212> PRT

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<220>

<223> human CLASP-7

<400> 92

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			20				25						30			
Pro	His	Ser	Ser	Arg	Arg	Cys	Ser	Ser	Ser	Leu	Gly	Val	Pro	Leu	Thr	
		35				40						45				
Glu	Val	Val	Glu	Pro	Leu	Asp	Phe	Glu	Asp	Val	Leu	Leu	Ser	Arg	Pro	
	50					55					60					
Pro	Asp	Ala	Glu	Pro	Gly	Pro	Leu	Arg	Asp	Leu	Val	Glu	Phe	Pro	Ala	
	65				70					75					80	
Asp	Asp	Leu	Glu	Leu	Leu	Leu	Gln	Pro	Arg	Glu	Cys	Arg	Thr	Thr	Glu	
				85					90						95	
Pro	Gly	Ile	Pro	Lys	Asp	Glu	Lys	Leu	Asp	Ala	Gln	Val	Arg	Ala	Ala	
			100					105					110			
Val	Glu	Met	Tyr	Ile	Glu	Asp	Trp	Val	Ile	Val	His	Arg	Arg	Tyr	Gln	
		115					120					125				
Tyr	Leu	Ser	Ala	Ala	Tyr	Ser	Pro	Val	Thr	Thr	Asp	Thr	Gln	Arg	Glu	
	130					135					140					
Arg	Gln	Lys	Gly	Leu	Pro	Arg	Gln	Val	Phe	Glu	Gln	Asp	Ala	Ser	Gly	
	145				150					155					160	
Asp	Glu	Arg	Ser	Gly	Pro	Glu	Asp	Ser	Asn	Asp	Ser	Arg	Arg	Gly	Ser	
				165					170					175		
Gly	Ser	Pro	Glu	Asp	Thr	Pro	Arg	Ser	Ser	Gly	Ala	Ser	Ser	Ile	Phe	
			180					185					190			
Asp	Leu	Arg	Asn	Leu	Ala	Ala	Asp	Ser	Leu	Leu	Pro	Ser	Leu	Leu	Glu	
		195					200					205				
Arg	Ala	Ala	Pro	Glu	Asp	Val	Asp	Arg	Arg	Asn	Glu	Thr	Leu	Arg	Arg	
	210					215					220					
Gln	His	Arg	Pro	Pro	Ala	Leu	Leu	Thr	Leu	Tyr	Pro	Ala	Pro	Asp	Glu	
	225				230					235					240	

Glu	Ile	Glu	Pro	Ile	Phe	Gly	Ile	Leu	Ala	Leu	Tyr	Asp	Val	Arg	Glu	275	280	285
Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu	Asn	Ser	Asp	Ser	290	295	300
Met	Lys	Gly	Leu	Leu	Arg	Ala	His	Gly	Thr	His	Pro	Ala	Ile	Ser	Thr	305	310	315
Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Val	Thr	Tyr	Pro	Ser	Pro	Asp	Ile	325	330	335
Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	Gly	Asp	Ile	Ser	340	345	350
Glu	Cys	Cys	Glu	Pro	Tyr	Met	Val	Leu	Lys	Glu	Val	Asp	Thr	Ala	Lys	355	360	365
Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Arg	Leu	Ala	Ala	Glu	Gln	Phe	Cys	370	375	380
Thr	Arg	Leu	Gly	Arg	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Thr	Ala	Val	His	385	390	395
Leu	Ala	Asn	Ile	Val	Ser	Ser	Ala	Gly	Gln	Leu	Asp	Arg	Asp	Ser	Asp	405	410	415
Ser	Glu	Gly	Glu	Arg	Arg	Pro	Ala	Trp	Thr	Asp	Arg	Arg	Arg	Arg	Gly	420	425	430
Pro	Gln	Asp	Arg	Ala	Ser	Ser	Gly	Asp	Asp	Ala	Cys	Ser	Phe	Ser	Gly	435	440	445
Phe	Arg	Pro	Ala	Thr	Leu	Thr	Val	Thr	Asn	Phe	Phe	Lys	Gln	Glu	Ala	450	455	460
Glu	Arg	Leu	Ser	Asp	Glu	Asp	Leu	Phe	Lys	Phe	Leu	Ala	Asp	Met	Arg	465	470	475
Arg	Pro	Ser	Ser	Leu	Leu	Arg	Arg	Leu	Arg	Pro	Val	Thr	Ala	Gln	Leu	485	490	495
Lys	Ile	Asp	Ile	Ser	Pro	Ala	Pro	Glu	Asn	Pro	His	Phe	Cys	Leu	Ser	500	505	510
Pro	Glu	Leu	Leu	His	Ile	Lys	Pro	Tyr	Pro	Asp	Pro	Arg	Gly	Arg	Pro	515	520	525
Thr	Lys	Glu	Ile	Leu	Glu	Phe	Pro	Ala	Arg	Glu	Val	Tyr	Ala	Pro	His	530	535	540
Thr	Ser	Tyr	Arg	Asn	Leu	Leu	Tyr	Val	Tyr	Pro	His	Ser	Leu	Asn	Phe	545	550	555

Ser	Ser	Cys	Ser	Glu	Phe	Thr	Arg	Glu	Ala	Phe	Thr	Pro	Val	Val	Tyr
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His	Asn	Lys	Ser	Pro	Glu	Phe	Tyr	Glu	Glu	Phe	Lys	Leu	His	Leu	Pro
	610					615					620				
Ala	Cys	Val	Thr	Glu	Asn	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val
625					630					635					640
Ser	Cys	Gln	Pro	Arg	Pro	Gly	Thr	Ala	Leu	Glu	Thr	Pro	Val	Gly	Phe
				645					650					655	
Thr	Trp	Ile	Pro	Leu	Leu	Gln	His	Gly	Arg	Leu	Arg	Thr	Gly	Pro	Phe
			660					665					670		
Cys	Leu	Pro	Val	Ser	Val	Asp	Gln	Pro	Pro	Pro	Ser	Tyr	Ser	Val	Leu
		675					680					685			
Thr	Pro	Asp	Val	Ala	Leu	Pro	Gly	Met	Arg	Trp	Val	Asp	Gly	His	Lys
	690					695					700				
Gly	Val	Phe	Ser	Val	Glu	Leu	Thr	Ala	Val	Ser	Ser	Val	His	Pro	Gln
705					710					715					720
Asp	Pro	Tyr	Leu	Asp	Lys	Phe	Phe	Thr	Leu	Val	His	Val	Leu	Glu	Glu
				725					730					735	
Gly	Ala	Phe	Pro	Phe	Arg	Leu	Lys	Asp	Thr	Val	Leu	Ser	Glu	Gly	Asn
			740					745					750		
Val	Glu	Gln	Glu	Leu	Arg	Ala	Ser	Leu	Ala	Ala	Leu	Arg	Leu	Ala	Ser
		755					760					765			
Pro	Glu	Pro	Leu	Val	Ala	Phe	Ser	His	His	Val	Leu	Asp	Lys	Leu	Val
	770					775					780				
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785					790					795					800
Gly	Arg	Gly	Ala	Phe	Glu	Ala	Met	Ala	His	Val	Val	Ser	Leu	Val	His
				805					810					815	
Arg	Ser	Leu	Glu	Ala	Ala	Gln	Asp	Ala	Arg	Gly	His	Cys	Pro	Gln	Leu
			820					825					830		
Ala	Ala	Tyr	Val	His	Tyr	Ala	Phe	Arg	Leu	Pro	Gly	Thr	Glu	Pro	Ser
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Leu	Pro	Asp	Gly	Ala	Pro	Pro	Val	Thr	Val	Gln	Ala	Ala	Thr	Leu	Ala
	850					855					860				
Arg	Gly	Ser	Gly	Arg	Pro	Ala	Ser	Leu	Tyr	Leu	Ala	Arg	Ser	Lys	Ser
865					870					875					880

Ala	Leu	Gln	Trp	Val	Val	Ser	Ser	Ser	Ala	Val	Arg	Glu	Ala	Ile	Leu
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Gln	His	Ala	Trp	Phe	Phe	Phe	Gln	Leu	Met	Val	Lys	Ser	Met	Ala	Leu
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His	Leu	Leu	Leu	Gly	Gln	Arg	Leu	Asp	Thr	Pro	Arg	Lys	Leu	Arg	Phe
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Leu	Glu	Val	Ile	Thr	Arg	Val	His	Lys	Asp	Val	Glu	Leu	Ala	Glu	His
		980						985					990		
Leu	Asn	Ala	Ser	Leu	Ala	Phe	Phe	Leu	Ser	Asp	Leu	Leu	Ser	Leu	Val
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Asp	Arg	Gly	Phe	Val	Phe	Ser	Leu	Val	Arg	Ala	His	Tyr	Lys	Gln	Val
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Ala	Thr	Arg	Leu	Gln	Ser	Ser	Pro	Asn	Pro	Ala	Ala	Leu	Leu	Thr	Leu
1025				1030					1035					1040	
Arg	Met	Glu	Phe	Thr	Arg	Ile	Leu	Cys	Ser	His	Glu	His	Tyr	Val	Thr
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Leu	Asn	Leu	Pro	Cys	Cys	Pro	Leu	Ser	Pro	Pro	Ala	Ser	Pro	Ser	Pro
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Ser	Val	Ser	Ser	Thr	Thr	Ser	Gln	Ser	Ser	Thr	Phe	Ser	Ser	Gln	Ala
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Pro	Asp	Pro	Lys	Val	Thr	Ser	Met	Phe	Glu	Leu	Ser	Gly	Pro	Phe	Arg
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Gln	Gln	His	Phe	Leu	Ala	Gly	Leu	Leu	Leu	Thr	Glu	Leu	Ala	Leu	Ala
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Leu	Gln	Glu	Asp	Gln	Asp	Val	Arg	His	Leu	Ala	Leu	Ala	Val	Leu	Lys
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Lys	Gln	Ala	Gln	Ile	Ala	Ser	Leu	Tyr	Met	Pro	Leu	Tyr	Gly	Met	Leu
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 Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu Tyr Lys  
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 Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu Met Arg  
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 Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met Gln Val  
 1490 1495 1500  
 Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe Ser Glu  
 1505 1510 1515 1520

Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu	1555	1560	1565
His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala	1570	1575	1580
Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn	1585	1590	1595 1600
Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln	1605	1610	1615
Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu	1620	1625	1630
Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile	1635	1640	1645
Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser	1650	1655	1660
Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly	1665	1670	1675 1680
Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly	1685	1690	1695
Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu	1700	1705	1710
Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu	1715	1720	1725
Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg	1730	1735	1740
Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly	1745	1750	1755 1760
Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys	1765	1770	1775
Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe	1780	1785	1790
Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys	1795	1800	1805
Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu	1810	1815	1820
Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp	1825	1830	1835 1840

Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg  
1875 1880 1885

Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile  
1890 1895 1900

Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln  
1905 1910 1915 1920

Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val  
1925 1930 1935

Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu  
1940 1945 1950

Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu  
1955 1960 1965

Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala Leu Arg  
1970 1975 1980

Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu  
1985 1990 1995 2000

Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu  
2005 2010 2015

Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg  
2020 2025 2030

Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu  
2035 2040 2045

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Lys Lys Arg Arg Thr Val Arg Arg Val Ile Gln Glu Glu Phe His Arg  
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Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu  
35 40 45

Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln  
50 55 60

Arg Asp Thr Arg Thr Leu Lys Thr Thr Val Thr Thr Asp Thr Thr Thr  
65 70 75

Lys	Ala	Glu	Asn	Leu	Leu	Val	Lys	Glu	Ala	Cys	Lys	Phe	Tyr	Ser	Ser	100	105	110
Gln	Trp	His	Val	Val	Asn	Tyr	Lys	Tyr	Glu	Gln	Tyr	Ser	Gly	Asp	Ile	115	120	125
Arg	Gln	Leu	Pro	Arg	Ala	Glu	Tyr	Lys	Pro	Glu	Lys	Leu	Pro	Ser	His	130	135	140
Ser	Phe	Glu	Ile	Asp	His	Glu	Asp	Ala	Asp	Lys	Asp	Glu	Asp	Thr	Thr	145	150	155
Ser	His	Ser	Ser	Ser	Lys	Gly	Gly	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Val	165	170	175
Phe	Lys	Ser	Gly	Trp	Leu	Tyr	Lys	Gly	Asn	Phe	Asn	Ser	Thr	Val	Asn	180	185	190
Asn	Thr	Val	Thr	Val	Arg	Ser	Phe	Lys	Lys	Arg	Tyr	Phe	Gln	Leu	Thr	195	200	205
Gln	Leu	Pro	Asp	Asn	Ser	Tyr	Ile	Met	Asn	Phe	Tyr	Lys	Asp	Glu	Lys	210	215	220
Ile	Ser	Lys	Glu	Pro	Lys	Gly	Cys	Ile	Phe	Leu	Asp	Ser	Cys	Thr	Gly	225	230	235
Val	Val	Gln	Asn	Asn	Arg	Leu	Arg	Lys	Tyr	Ala	Phe	Glu	Leu	Lys	Met	245	250	255
Asn	Asp	Leu	Thr	Tyr	Phe	Val	Leu	Ala	Ala	Glu	Thr	Glu	Ser	Asp	Met	260	265	270
Asp	Glu	Trp	Ile	His	Thr	Leu	Asn	Arg	Ile	Leu	Gln	Ile	Ser	Pro	Glu	275	280	285
Gly	Pro	Leu	Gln	Gly	Arg	Arg	Ser	Thr	Glu	Leu	Thr	Asp	Leu	Gly	Leu	290	295	300
Asp	Ser	Leu	Asp	Asn	Ser	Val	Thr	Cys	Glu	Cys	Thr	Pro	Glu	Glu	Thr	305	310	315
Asp	Ser	Ser	Glu	Asn	Asn	Leu	His	Ala	Asp	Phe	Ala	Lys	Tyr	Leu	Thr	325	330	335
Glu	Thr	Glu	Asp	Thr	Val	Lys	Thr	Thr	Arg	Asn	Met	Glu	Arg	Leu	Asn	340	345	350
Leu	Phe	Ser	Leu	Asp	Pro	Asp	Ile	Asp	Thr	Leu	Lys	Leu	Gln	Lys	Lys	355	360	365
Asp	Leu	Leu	Glu	Pro	Glu	Ser	Val	Ile	Lys	Pro	Phe	Glu	Glu	Lys	Ala	370	375	380

Phe	Phe	Val	Ser	Val	Ala	Leu	Tyr	Asp	Leu	Arg	Asp	Ser	Arg	Lys	Ile
		420						425					430		
Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Ala	Ala	Val	Arg	Gln	Met
		435					440					445			
Leu	Leu	Gly	Ala	Ser	Val	Ala	Leu	Glu	Asn	Gly	Asn	Ile	Asp	Thr	Ile
	450					455					460				
Thr	Pro	Arg	Gln	Ser	Glu	Glu	Pro	His	Ile	Lys	Gly	Leu	Pro	Glu	Glu
465					470					475				480	
Trp	Leu	Lys	Phe	Pro	Lys	Gln	Ala	Val	Phe	Ser	Val	Ser	Asn	Pro	His
				485					490					495	
Ser	Glu	Ile	Val	Leu	Val	Ala	Lys	Ile	Glu	Lys	Val	Leu	Met	Gly	Asn
			500					505					510		
Ile	Ala	Ser	Gly	Ala	Glu	Pro	Tyr	Ile	Lys	Asn	Pro	Asp	Ser	Asn	Lys
		515					520					525			
Tyr	Ala	Gln	Lys	Ile	Leu	Lys	Ser	Asn	Arg	Gln	Phe	Cys	Ser	Lys	Leu
	530					535					540				
Gly	Lys	Tyr	Arg	Arg	Ala	Phe	Ala	Trp	Ala	Val	Arg	Ser	Val	Phe	Lys
545					550					555				560	
Asp	Asn	Gln	Gly	Asn	Val	Asp	Arg	Asp	Ser	Arg	Phe	Ser	Pro	Leu	Phe
				565					570					575	
Arg	Gln	Glu	Ser	Ser	Lys	Ile	Ser	Thr	Glu	Asp	Leu	Val	Lys	Leu	Val
			580					585					590		
Ser	Asp	Tyr	Arg	Arg	Ala	Asp	Arg	Ile	Ser	Lys	Met	Gln	Thr	Ile	Pro
		595					600					605			
Gly	Ser	Leu	Asp	Ile	Ala	Val	Asp	Asn	Val	Pro	Leu	Glu	His	Pro	Asn
	610					615					620				
Cys	Val	Thr	Ser	Ser	Phe	Ile	Pro	Val	Lys	Pro	Phe	Asn	Met	Met	Ala
625					630					635				640	
Gln	Thr	Glu	Pro	Thr	Val	Glu	Val	Glu	Glu	Phe	Val	Tyr	Asp	Ser	Thr
				645				650						655	
Lys	Tyr	Cys	Arg	Pro	Tyr	Arg	Val	Tyr	Lys	Asn	Gln	Ile	Tyr	Ile	Tyr
			660					665					670		
Pro	Lys	His	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Cys	Phe	Asn	Lys	Ala	Arg
		675					680					685			
Asn	Ile	Thr	Val	Cys	Ile	Glu	Phe	Lys	Asn	Ser	Asp	Glu	Glu	Ser	Ala
	690					695					700				

Ser	Asp	Glu	Val	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	740	745	750
His	Ile	Leu	Phe	Ser	Phe	Tyr	His	Val	Thr	Cys	Asp	Ile	Asn	Ala	Lys	755	760	765
Ala	Asn	Ala	Lys	Lys	Lys	Glu	Ala	Leu	Glu	Thr	Ser	Val	Gly	Tyr	Ala	770	775	780
Trp	Leu	Pro	Leu	Met	Lys	His	Asp	Gln	Ile	Ala	Ser	Gln	Glu	Tyr	Asn	785	790	795
Ile	Pro	Ile	Ala	Thr	Ser	Leu	Pro	Pro	Asn	Tyr	Leu	Ser	Phe	Gln	Asp	805	810	815
Ser	Ala	Ser	Gly	Lys	His	Gly	Gly	Ser	Asp	Ile	Lys	Trp	Val	Asp	Gly	820	825	830
Gly	Lys	Pro	Leu	Phe	Lys	Val	Ser	Thr	Phe	Val	Val	Ser	Thr	Val	Asn	835	840	845
Thr	Gln	Asp	Pro	His	Val	Asn	Ala	Phe	Phe	Gln	Glu	Cys	Gln	Lys	Arg	850	855	860
Glu	Lys	Asp	Met	Ser	Gln	Ser	Pro	Thr	Ser	Asn	Phe	Ile	Arg	Ser	Cys	865	870	875
Lys	Asn	Leu	Leu	Asn	Val	Glu	Lys	Ile	His	Ala	Ile	Met	Ser	Phe	Leu	885	890	895
Pro	Ile	Ile	Leu	Asn	Gln	Leu	Phe	Lys	Val	Leu	Val	Gln	Asn	Glu	Glu	900	905	910
Asp	Glu	Ile	Thr	Thr	Thr	Val	Thr	Arg	Val	Leu	Pro	Asp	Ile	Val	Ala	915	920	925
Lys	Cys	His	Glu	Glu	Gln	Leu	Asp	His	Ser	Val	Gln	Ser	Tyr	Ile	Lys	930	935	940
Phe	Val	Phe	Lys	Thr	Arg	Ala	Cys	Lys	Glu	Arg	Pro	Val	His	Glu	Asp	945	950	955
Leu	Ala	Lys	Asn	Val	Thr	Gly	Leu	Leu	Lys	Ser	Asn	Asp	Ser	Pro	Thr	965	970	975
Val	Lys	His	Val	Leu	Lys	His	Ser	Trp	Phe	Phe	Phe	Ala	Ile	Ile	Leu	980	985	990
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Asp	Thr	Asn	Lys	Ile	Gln	Leu	Pro	995	1000	1005
Arg	Pro	Gln	Arg	Phe	Pro	Glu	Ser	Tyr	Gln	Asn	Glu	Leu	Asp	Asn	Leu	1010	1015	1020

Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn			
1060	1065	1070	
Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr			
1075	1080	1085	
Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro			
1090	1095	1100	
Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro			
1105	1110	1115	1120
Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser			
1125	1130	1135	
Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu			
1140	1145	1150	
Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu			
1155	1160	1165	
Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp			
1170	1175	1180	
Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met			
1185	1190	1195	1200
Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys			
1205	1210	1215	
Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp			
1220	1225	1230	
Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His			
1235	1240	1245	
Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile			
1250	1255	1260	
Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser			
1265	1270	1275	1280
Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys			
1285	1290	1295	
Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala			
1300	1305	1310	
Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr			
1315	1320	1325	
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr			
1330	1335	1340	

Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val  
 1380 1385 1390

Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys  
 1395 1400 1405

Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His  
 1410 1415 1420

Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly  
 1425 1430 1435 1440

Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr  
 1445 1450 1455

Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr  
 1460 1465 1470

Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val  
 1475 1480 1485

Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys  
 1490 1495 1500

Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe  
 1505 1510 1515 1520

Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu  
 1525 1530 1535

Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala  
 1540 1545 1550

Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His  
 1555 1560 1565

Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe  
 1570 1575 1580

Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser  
 1585 1590 1595 1600

His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly  
 1605 1610 1615

Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe  
 1620 1625 1630

Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val  
 1635 1640 1645

Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln  
 1650 1655 1660

Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu	1700	1705	1710
Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu	1715	1720	1725
Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu	1730	1735	1740
Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr	1745	1750	1755
Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser	1765	1770	1775
Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly	1780	1785	1790
Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr	1795	1800	1805
Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala	1810	1815	1820
Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe	1825	1830	1835
Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys	1845	1850	1855
Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr	1860	1865	1870
Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Lys	1875	1880	1885
Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser	1890	1895	1900
Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val	1905	1910	1915
Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro	1925	1930	1935
Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu	1940	1945	1950
Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile	1955	1960	1965
Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His	1970	1975	1980

Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg  
2020 2025 2030

Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met  
2035 2040 2045

Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn  
2050 2055 2060

Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala  
2065 2070 2075 2080

Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg  
2085 2090 2095

Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu  
2100 2105 2110

Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr  
2115 2120 2125

Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr  
2130 2135 2140

Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg  
2145 2150 2155 2160

Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser  
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Ser Ala Glu Val  
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<220>
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Pro Xaa Glu Xaa Ala Ile Xaa Xaa Xaa
  1             5

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<213> Artificial Sequence

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29

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28